

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 8, 2004, 18:14:16 ; Search time 155 Seconds  
(without alignments)  
733.659 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost		
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec		
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec		
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec		
5	1685	100.0	317	3	AAy84417	Aay84417 Amino aci		
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec		
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful		
8	1685	100.0	317	5	ABB08134	Abb08134 Human RAN		
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN		

10	1685	100.0	317	5	ABG31631	Abg31631	Human	RAN
11	1685	100.0	317	5	AAU78285	Aau78285	Human	TRA
12	1685	100.0	317	5	AAO19096	Aao19096	C neoform	
13	1685	100.0	317	6	ABP55108	Abp55108	Human	ost
14	1685	100.0	317	6	AAE34364	Aae34364	Human	rec
15	1685	100.0	317	6	ABR42314	Abr42314	Human	RAN
16	1685	100.0	317	7	ADB16988	Adb16988	Human	rec
17	1685	100.0	317	7	ADC35204	Adc35204	Human	TNF
18	1685	100.0	317	7	ADC73002	Adc73002	Human	RAN
19	1685	100.0	317	7	ADC78268	Adc78268	Human	RAN
20	1685	100.0	317	7	ABW02277	Abw02277	Human	RAN
21	1685	100.0	317	7	ADG46723	Adg46723	Human	RAN
22	1685	100.0	317	7	ADJ82112	Adj82112	Protein	f
23	1685	100.0	317	8	ADM96241	Adm96241	Human	rec
24	1677	99.5	317	2	AAW83018	Aaw83018	Osteoclas	
25	1422	84.4	270	7	ADJ82113	Adj82113	Protein	f
26	1417.5	84.1	316	2	AAW83017	Aaw83017	Osteoclas	
27	1417.5	84.1	316	2	AAW83194	Aaw83194	Human	ost
28	1417.5	84.1	316	2	AAW59654	Aaw59654	Amino	aci
29	1417.5	84.1	316	2	AAI17874	Aay17874	Murine	TR
30	1417.5	84.1	316	3	AAI91024	Aay91024	Mouse	OBM
31	1417.5	84.1	316	3	AAI84418	Aay84418	Amino	aci
32	1417.5	84.1	316	3	AAI84419	Aay84419	Amino	aci
33	1417.5	84.1	316	5	AAU78289	Aau78289	Mouse	TRA
34	1417.5	84.1	316	6	ABR42071	Abr42071	Human	RAN
35	1417.5	84.1	316	6	ABB99477	Abb99477	Amino	aci
36	1417.5	84.1	316	6	ABU08463	Abu08463	Amino	aci
37	1417.5	84.1	316	6	ABR55560	Abr55560	Amino	aci
38	1396.5	82.9	318	4	AAB82092	Aab82092	Rat	osteo
39	1326.5	78.7	294	2	AAW69956	Aaw69956	NF-kB	rec
40	1326.5	78.7	294	2	AAW68292	Aaw68292	NF-kB	rec
41	1326.5	78.7	294	2	AAE08737	Aae08737	Murine	re
42	1326.5	78.7	294	4	AAE04425	Aae04425	Murine	re
43	1326.5	78.7	294	4	AAE01992	Aae01992	Murine	RA
44	1326.5	78.7	294	5	AAE26102	Aae26102	Mouse	RAN
45	1326.5	78.7	294	7	ADB16986	Adb16986	Murine	re

#### ALIGNMENTS

##### RESULT 1

AAW83195

ID AAW83195 standard; protein; 317 AA.

XX

AC AAW83195;

XX

DT 11-FEB-1999 (first entry)

XX

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.insert.

XX

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;

KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;

KW hypercalcaemia; osteoclast differentiation and activation receptor;

KW Paget's disease.

XX

OS Homo sapiens.

XX  
 PN WO9846751-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 15-APR-1998; 98WO-US007584.  
 XX  
 PR 16-APR-1997; 97US-00842842.  
 PR 23-JUN-1997; 97US-00880855.  
 PR 30-MAR-1998; 98US-00052521.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ;  
 XX  
 DR WPI; 1998-594578/50.  
 DR N-PSDB; AAV70285.  
 XX  
 PT Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g.  
 PT treating bone diseases by modulating osteoclast differentiation and for  
 PT diagnosis.  
 XX  
 PS Claim 19; Fig 4; 47pp; English.  
 XX  
 CC The present sequence is human osteoprotegerin (OPG) binding protein. Host  
 CC cells transfected with vectors containing nucleic acid molecules encoding  
 CC OPG binding protein are used to produce recombinant OPG binding protein.  
 CC OPG binding protein is used in binding assays to determine osteoprotegrin  
 CC (OG) in biological samples; to screen for specific binding agents  
 CC (particularly agonists and antagonists, including intracellular proteins)  
 CC ; to raise Ab (useful in immunoassays for detection of OPG binding  
 CC protein) and to identify compounds that modulate binding of OPG binding  
 CC protein to osteoclast differentiation and activation receptor (ODAR). The  
 CC nucleic acid molecule encoding OPG binding protein can be used to detect  
 CC OPG binding protein-encoding sequences, e.g. screening for related  
 CC sequences, also to produce transgenic animal models, while complementary  
 CC sequences are used for antisense regulation of OPG binding protein  
 CC expression. Modulators of OPG binding protein, particularly soluble forms  
 CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,  
 CC e.g. osteoporosis, bone loss caused by arthritis or metastases,  
 CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,  
 CC loosening of prostheses, optionally in combination with agents that  
 CC promote bone growth  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

AAW69957

ID AAW69957 standard; protein; 317 AA.

XX

AC AAW69957;

XX

DT 08-OCT-1998 (first entry)

XX

DE NF-kB receptor activator RANK ligand (RANKL).

XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis; RANKL;

KW RANK ligand; tumour necrosis factor; TNF.

XX

OS Homo sapiens.

XX

PN WO9828426-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US023775.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Anderson DM, Galibert LJ, Maraskovsky E;

XX

DR WPI; 1998-377657/32.

DR N-PSDB; AAV41378.

XX

PT New isolated ligand for receptor activator of NF-kappa B - used to  
 PT develop products for augmenting an immune response for inhibiting an  
 PT inflammatory response and for protection of cells.

XX

PS Claim 27; Page 59-60; 80pp; English.

XX



CC This represents a human RANKL, a ligand for the RANK (receptor activator  
 CC of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the  
 CC tumour necrosis factor (TNF) family. A soluble RANK may be used for  
 CC inhibiting activation of NF-kB, by contacting a cell expressing membrane-  
 CC associated RANK with a soluble RANK which binds to RANK ligand (RANKL).  
 CC RANKL polypeptides can activate RANK and can be used to induce maturation  
 CC of dendritic cells and enhance their allo-stimulatory capacity, thereby  
 CC augmenting an immune response. The soluble RANK polypeptide composition  
 CC may also be used for regulating an immune or inflammatory response.  
 CC Inhibition of NF-kB by RANK antagonists may be useful in ameliorating  
 CC negative effects of an inflammatory response that result from triggering  
 CC of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host  
 CC reactions, or acute inflammatory reactions. They can also be used in  
 CC adjunct therapy for disease characterised by neoplastic cells that  
 CC express RANK. RANKL polypeptides can also be used to identify inhibitors  
 CC of RANK and thus inhibitors of an inflammatory response, and also for  
 CC protecting RANK-expressing cells from the negative effects of  
 CC chemotherapy or the presence of high levels of TNF-alpha. The products  
 CC can also be used for detection and drug screening  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
  
 Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLD 300  
  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 3  
 AAW68293  
 ID AAW68293 standard; protein; 317 AA.  
 XX  
 AC AAW68293;  
 XX

DT 08-OCT-1998 (first entry)  
 XX  
 DE NF-kB receptor activator RANK ligand (RANKL).  
 XX  
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 KW immune response; inflammatory response; toxic shock; sepsis; RANKL;  
 KW RANK ligand; tumour necrosis factor; TNF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9828424-A2.  
 XX  
 PD 02-JUL-1998.  
 XX  
 PF 22-DEC-1997; 97WO-US023866.  
 XX  
 PR 23-DEC-1996; 96US-0059978P.  
 PR 07-MAR-1997; 97US-00813509.  
 PR 14-OCT-1997; 97US-0064671P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Galibert LJ, Maraskovsky E;  
 XX  
 DR WPI; 1998-377655/32.  
 DR N-PSDB; AAV41372.  
 XX  
 PT New isolated receptor activator of necrosis factor-kappa B - useful for,  
 PT e.g. developing products for regulating an immune or inflammatory  
 PT response, treating toxic shock or sepsis.  
 XX  
 PS Example 7; Page 59-60; 80pp; English.  
 XX  
 CC This represents a human RANKL, a ligand for the RANK (receptor activator  
 CC of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the  
 CC tumour necrosis factor (TNF) family. Host cells transformed or  
 CC transfected with an expression vector comprising the RANK encoding  
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble  
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell  
 CC expressing membrane-associated RANK with a soluble RANK which binds to  
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be  
 CC used for regulating an immune or inflammatory response. Inhibition of NF-  
 CC kB by RANK antagonists may be useful in ameliorating negative effects of  
 CC an inflammatory response that result from triggering of RANK, e.g. in  
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute  
 CC inflammatory reactions. They can also be used in adjunct therapy for  
 CC disease characterised by neoplastic cells that express RANK. The products  
 CC can also be used for detection and drug screening  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
 |||

Database	Accession	Sequence	Length
Db	1	MRRASRDYTKYLGRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTinATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTinATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMtFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMtFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGGFFKLRSgEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHfYSINVGGFFKLRSgEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDODATYFGAFKVRDID	317

AAE08738

ID AAE08738 standard; protein; 317 AA.

XX

AC AAE08738;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human receptor activator of NF kappaB ligand (RANKL) protein.

XX

KW Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF;

KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;

KW immune response; inflammatory response; graft-versus-host reaction;

KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;  
KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX

OS Homo sapiens.

XX

PN US6271349-B1.

XX

PD 07-AUG-2001.

XX

PF 17-DEC-1998; 98US-00215649.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 23-DEC-1996; 96US-00772330.

PR 07-MAR-1997; 97US-0077181P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Dougall WC, Galibert L;

XX WPI; 1998-377655/32.  
DR N-PSDB; AAD15311.  
XX  
PT New isolated receptor activator of necrosis factor-kappa B - useful for,  
PT e.g. developing products for regulating an immune or inflammatory  
PT response, treating toxic shock or sepsis.  
XX  
PS Example 15; Col 71-72; 47pp; English.  
XX  
CC The patent discloses novel receptor activator of nuclear factor (NF)-  
CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of  
CC the tumour necrosis factor (TNF) receptor superfamily and associates with  
CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the  
CC regulation of immune and inflammatory response. The receptors are useful  
CC for regulating immune response and in screening for inhibitors of these  
CC receptors. The cytoplasmic domain of RANK is used in developing assays  
CC for inhibitors of signal transduction, e.g. for screening the molecules  
CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and  
CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful  
CC in ameliorating the negative effects of an inflammatory response that  
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
CC graft-versus-host reactions, acute inflammatory reactions and the effects  
CC of bone resorption. RANK acts as an anti- apoptotic signal and rescue the  
CC cells that express RANK from apoptosis. Soluble forms of the receptor are  
CC used in vivo or in vitro based screening tests for agonists or  
CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B  
CC activation, or to inhibit transduction of a signal via RANK. RANK  
CC compositions are used in the development of both agonistic and  
CC antagonistic antibodies, or as an adjunct therapy for disease  
CC characterised by neoplastic cells that express RANK. Compounds that  
CC interfere with RANK/TRAF6 interactions are useful for modulating the  
CC formation of osteoclasts from osteoclast precursors and for modulating  
CC osteoclast function and activities. They are used as inhibitors of  
CC diseases associated with excess bone resorption and as immunosuppressants  
CC or anti-inflammatory agents. The RANK DNAs are useful for the expression  
CC of recombinant proteins, as probes for analysis of the presence or  
CC distribution of RANK transcripts, while the proteins are useful in  
CC preparing kits for the detection of soluble RANK, or monitor RANK-related  
CC activity. The present sequence is RANK ligand (RANKL) protein from human  
XX  
SQ Sequence 317 AA;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFahlTINATDIPSGSH	180

Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 Qy 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

AA Y84417

ID AAY84417 standard; protein; 317 AA.

XX

AC AAY84417;

XX

DT 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

KW tumour necrosis factor receptor; type II transmembrane protein;

KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;

KW osteoporosis; bone resorption.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 49. .69

FT /note= "transmembrane region"

FT Domain 70. .157

FT /note= "extracellular stalk domain"

FT Region 158. .317

FT /note= "active ligand moiety"

XX

PN WO200015807-A1.

XX

PD 23-MAR-2000.

XX

PF 13-SEP-1999; 99WO-DK000481.

XX

PR 15-SEP-1998; 98DK-00001164.

PR 02-OCT-1998; 98US-0102896P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Halkier T, Haaning J;

XX

DR WPI; 2000-271444/23.

DR N-PSDB; AAZ99964.

XX

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to

PT treat, prevent and ameliorate osteoporosis.

XX

PS Claim 19; Page 78-79; 110pp; English.

XX

CC The present sequence represents a human osteoprotegerin ligand (OPGL).  
CC Osteoprotegerin is a secreted member of the tumour necrosis factor  
CC receptor family, which blocks osteoclastogenesis in a dose dependent  
CC manner. The OPGL protein is synthesised as a type II transmembrane  
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL  
CC is a potent osteoclast differentiation factor when combined with CSF-1.  
CC It is not capable of inducing osteoclast differentiation in the absence  
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The  
CC specification describes a method for the in vivo down-regulation of OPGL  
CC activity in an animal. The method comprises using at least one OPGL  
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce  
CC an immune response in the animal. The method and OPGL polypeptide are  
CC useful for treating, preventing and ameliorating osteoporosis or other  
CC diseases or conditions characterised by excessive bone resorption

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 3; Length 317;

Best Local Similarity 100.0%; Pred. No. 6.2e-154;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

|||||

Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

|||||

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

|||||

Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

|||||

Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300

|||||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317

|||||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 6

AAE04426

ID AAE04426 standard; protein; 317 AA.

XX

AC AAE04426;

XX

DT 04-SEP-2001 (first entry)

XX  
 DE Human receptor activator of NF- $\chi$  B ligand (huRANKL) protein.  
 XX  
 KW Human; receptor activator of NF- $\chi$  B; RANK; tumour necrosis factor; TNF;  
 KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response;  
 KW chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 162. .317  
 FT /note= "Receptor binding region"  
 XX  
 PN US6242213-B1.  
 XX  
 PD 05-JUN-2001.  
 XX  
 PF 22-DEC-1997; 97US-00995659.  
 XX  
 PR 23-DEC-1996; 96US-0059978P.  
 PR 23-DEC-1996; 96US-00772330.  
 PR 07-MAR-1997; 97US-0077181P.  
 PR 14-OCT-1997; 97US-0064671P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM;  
 XX  
 DR WPI; 2001-407216/43.  
 DR N-PSDB; AAD08715.  
 XX  
 PT New DNA molecules, useful for producing ligands (which are useful for  
 PT regulating immune response and in screening for inhibitors of NF- $\chi$  B  
 PT receptor activator) of the receptor activator of NF- $\chi$  B (RANK).  
 XX  
 PS Claim 1; Col 65-66; 43pp; English.  
 XX  
 CC The present invention relates to receptor activator of NF- $\chi$  B (RANK)  
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to  
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane  
 CC proteins respectively. RANK is a member of the tumour necrosis factor  
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular  
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2 and  
 CC TRAF3. The DNA molecules are useful for producing ligands of RANK. The  
 CC ligands are useful for regulating immune response and in screening for  
 CC inhibitors of RANK. The present sequence is human RANKL (huRANKL) protein  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 4; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

# RESULT 7

AAE01993

ID AAE01993 standard; protein; 317 AA.

XX

AC AAE01993;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human full-length RANKL (receptor activator of NF-kappaB ligand).

XX

KW Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;  
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;  
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;  
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;  
 KW immune system dysfunction; familial expansile osteolysis; FEO;  
 KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.

XX

OS Homo sapiens.

XX

PN WO200136637-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-US031459.

XX

PR 17-NOV-1999; 99US-00442029.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Anderson DM, Hughes AE;

XX

DR WPI; 2001-329222/34.

DR

N-PSDB; AAD05904.

XX

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the  
 PT treatment of Pagets disease and Familial Expansile Osteolysis (FEO).





ID ABB08134 standard; protein; 317 AA.  
 XX  
 AC ABB08134;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Human RANKL polypeptide.  
 XX  
 KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;  
 KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
 KW tuberculostatic; cytostatic; human; RANKL.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200236141-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 30-OCT-2001; 2001WO-US044834.  
 XX  
 PR 02-NOV-2000; 2000US-0245721P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;  
 PI Thomas EK;  
 XX  
 DR WPI; 2002-500114/53.  
 XX  
 PT Treating an individual suffering from infection, e.g. inflammation,  
 PT chickenpox or AIDS, by administering a combination of dendritic cell  
 PT mobilization factor or maturation agent, T cell enhancing factor and  
 PT antigen-specific T cells.  
 XX  
 PS Disclosure; Page 42-43; 43pp; English.  
 XX  
 CC The invention relates to treating an individual at risk for or suffering  
 CC from infection with a pathogenic or opportunistic organism. The method  
 CC involves administering a combination of two to five agents comprising:  
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation  
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;  
 CC or (e) activated, antigen-specific T cells. The methods are useful for  
 CC treating an individual at risk for or suffering from infection with a  
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria  
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.  
 CC T. cruzi, which causes Chaga's disease). The methods are especially  
 CC useful for treating an individual suffering from immunosuppression by  
 CC enhancing a lymphocyte-mediated immune response. In particular, the  
 CC method is useful for treating inflammations, chickenpox, oral or genital  
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T  
 CC cell leukemia or T cell lymphoma. The activated antigen-presenting  
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence  
 CC represents a human RANKL polypeptide fragment  
 XX  
 SQ Sequence 317 AA;

Query Match

100.0%; Score 1685; DB 5; Length 317;

Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180
      |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPSGSH 180

QY    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
      |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

QY    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
      |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

QY    301 PDQDATYFGAFKVRDID 317
      |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 9

AAE26103

ID AAE26103 standard; protein; 317 AA.

XX

AC AAE26103;

XX

DT 14-NOV-2002 (first entry)

XX

DE Human RANK ligand (RANKL) protein.

XX

KW Human; RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;

KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;

KW tumour necrosis factor receptor-associated factor; immunosuppressive;

KW antibacterial; antiinflammatory; chromosome 13.

XX

OS Homo sapiens.

XX

PN US2002086827-A1.

XX

PD 04-JUL-2002.

XX

PF 30-MAY-2001; 2001US-00871291.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-0077181P.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

PR 17-DEC-1999; 99US-00466496.

PR 24-MAY-2000; 2000US-00577800.

XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Anderson DM;  
XX  
DR WPI; 2002-642254/69.  
DR N-PSDB; AAD43213.  
XX  
PT A novel RANK (receptor activator of nuclear factor-kappaB (NF-kB))  
PT polypeptide, useful for inhibiting activation of NF-kB and for regulating  
PT an immune or inflammatory response in an individual.  
XX  
PS Example 15; Page 35; 49pp; English.  
XX  
CC The invention relates to novel RANK (receptor activator of nuclear factor  
CC -kappaB (NF-kB)) proteins and polynucleotides encoding them. Sequences of  
CC the invention are useful for inhibiting activation of NF-kappaB. They are  
CC useful for regulating an immune or inflammatory response in an individual  
CC at risk for an immune or inflammatory response. Inhibition of NF-kappaB  
CC by RANK antagonists is useful in ameliorating negative effects of an  
CC inflammatory response that results from triggering of RANK, for e.g. in  
CC treating toxic shock or sepsis, graft-versus-host reactions or acute  
CC inflammatory reactions. Soluble RANK is useful as an adjunct therapy for  
CC diseases characterised by neoplastic cells that express RANK. Soluble  
CC forms of the receptor are useful in vitro to screen for agonists or  
CC antagonists of RANK activity. The cytoplasmic domain of RANK is useful in  
CC developing assays for inhibitors of signal transduction, to screen for  
CC molecules that inhibit interaction of RANK with tumour necrosis factor  
CC receptor-associated factor (TRAF) 2 or TRAF3. The present sequence is  
CC human RANK ligand (RANKL) protein. RANKL gene is located on chromosome 13  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;  
Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300



Query Match 100.0%; Score 1685; DB 5; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317

```

RESULT 11

AAU78285

ID AAU78285 standard; protein; 317 AA.

XX

AC AAU78285;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human TRANCE protein splice variant 1.

XX

KW Human; tumour necrosis factor-related activation induced cytokine;

KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;

KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;

KW rheumatoid arthritis; acromegaly; gigantism; exostosis; carilageinea;

KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;

KW cartilage growth; skeletal growth.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 126. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 137. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 140. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 145. .317

FT /note= "Specifically claimed in claims 17 and 18"



```

Db          |||||
61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180
          |||||

Db          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
          |||||

Db          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||||

Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy          301 PDQDATYFGAFKVRDID 317
          |||||

Db          301 PDQDATYFGAFKVRDID 317

```

RESULT 12

AAO19096

ID AAO19096 standard; protein; 317 AA.

XX

AC AAO19096;

XX

DT 22-NOV-2002 (first entry)

XX

DE C neoformans antigen expressing dendritic cell related protein #5.

XX

KW Human; fungicide; fungal infection; dendritic cell; antigen;

KW Cryptococcus neoformans; vaccine; immunostimulant.

XX

OS Homo sapiens.

XX

PN WO200266053-A2.

XX

PD 29-AUG-2002.

XX

PF 14-DEC-2001; 2001WO-US048288.

XX

PR 04-JAN-2001; 2001US-0259653P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Thomas EK;

XX

DR WPI; 2002-674896/72.

XX

PT Producing a population of activated, Cryptococcus neoformans antigen-  
PT presenting dendritic cells for preventing or treating C. neoformans  
PT infection comprises causing the obtained dendritic cells to present the  
PT antigen.

XX

PS Disclosure; Page 30-32; 32pp; English.

XX

CC The present invention relates to a method of producing a population of





XX  
 FH Key Location/Qualifiers  
 FT Domain 1. .47  
 FT /note= "putative cytoplasmic domain"  
 FT Domain 48. .68  
 FT /note= "putative transmembrane signal-anchor"  
 FT Domain 69. .317  
 FT /note= "putative extracellular domain"  
 FT Modified-site 171  
 FT /note= "potential N-glycosylation site"  
 FT Modified-site 198  
 FT /note= "potential N-glycosylation site"  
 XX  
 PN WO200276507-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US001238.  
 XX  
 PR 23-MAR-2001; 2001US-0278215P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Grewal I;  
 XX  
 DR WPI; 2003-058352/05.  
 DR N-PSDB; ABV75842.  
 XX  
 PT Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,  
 PT useful for treating immune related disorders such as autoimmune disease,  
 PT rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.  
 XX  
 PS Claim 1; Fig 1B; 111pp; English.  
 XX  
 CC The present sequence is the protein sequence of human osteoprotegerin  
 CC ligand (OPGL), a member of the tumour necrosis factor (TNF) family of  
 CC molecules that has been reported to bind to at least 2 receptors, RANK  
 CC and OPG. In the present invention, OPGL was shown to activate human  
 CC monocytes, and to activate such monocytes to secrete certain cytokines  
 CC such as interleukin-1 (IL-1), IL-6, IL-12, MIP-1alpha and TNF-alpha and  
 CC chemokines such as IL-8. OPGL may function in up-regulation of co-  
 CC stimulatory molecules such as ICAM-a and VCAM-1, LFA, and B7.1, B7.3 and  
 CC B7h. OPGL may also serve as an antigen presenting molecule which enhances  
 CC T-cell activation. The invention provides methods of using OPGL to  
 CC activate monocytes to secrete chemokines or cytokines by exposing a  
 CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided  
 CC are methods of using OPGL to treat conditions or diseases in mammals  
 CC associated with, or resulting from lack of, or decreased, chemokine or  
 CC cytokine secretion by monocytes. The invention also provides agonist and  
 CC antagonist molecules to modulate immune activity. These may include  
 CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti-  
 CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor  
 CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin  
 CC is used in a claimed method of treating an immune-related condition,  
 CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent  
 CC diabetes, osteoarthritis, inflammatory bowel disease (especially  
 CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection

CC or allergy  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
      |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
      |||
Db    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300
      |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      |||
Db    301 PDQDATYFGAFKVRDID 317
```

RESULT 14

AAE34364

ID AAE34364 standard; protein; 317 AA.

XX

AC AAE34364;

XX

DT 14-MAY-2003 (first entry)

XX

DE Human receptor activator of NF-kappa B ligand (RANKL).

XX

KW Human; acute septic arthritis; osteomalacia; hyperparathyroidism;

KW Cushing's syndrome; receptor activator of NF-kappa B ligand; cancer;

KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;

KW monocostotic fibrous dysplasia; radiation therapy; spinal cord injury;

KW RANKL; Gaucher's disease; polyostotic fibrous dysplasia; scurvy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .47

FT /note= "Intracellular domain"

FT Domain 48. .68

FT /note= "Transmembrane domain"

FT Domain 69. .317

FT /note= "Extracellular domain"  
 FT Binding-site 162. .317  
 FT /note= "RANK-binding domain"  
 XX  
 PN WO200292016-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 17-MAY-2002; 2002WO-US016002.  
 XX  
 PR 17-MAY-2001; 2001US-0291919P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Dougall WC, Anderson DM;  
 XX  
 DR WPI; 2003-129220/12.  
 DR N-PSDB; AAD52598.  
 XX  
 PT Treating patients having e.g. acute septic arthritis, osteomalacia,  
 PT hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises  
 PT administering a receptor activator of NF-kappa B antagonist to increase  
 PT bone formation.  
 XX  
 PS Claim 1; Page 51-52; 52pp; English.  
 XX  
 CC The invention relates to a method of treating a patient having e.g. acute  
 CC septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome  
 CC or spinal cord injury. The method involves administering a receptor  
 CC activator of NF-kappa B (RANK) antagonist to stimulate an increase in the  
 CC rate for formation of new bone. RANK antagonist is capable of inhibiting  
 CC the ability of RANK to induce NF-kappa B. The method is useful for  
 CC stimulating bone formation, or for treating patients having acute septic  
 CC arthritis, osteomalacia (including rickets and scurvy),  
 CC hyperparathyroidism, Cushing's syndrome, monoostotic fibrous dysplasia,  
 CC polyostotic fibrous dysplasia, Gaucher's disease, Langerhan's cell  
 CC histiocytosis, spinal cord injury, patients requiring periodontal  
 CC reconstruction, or patients who have completed a course or radiation  
 CC therapy for cancer. The method is also useful for treating a patient who  
 CC is a prosthetic joint recipient, a bone graft recipient, or a ligament  
 CC graft recipient. The invention is useful in gene therapy. The present  
 CC sequence is human RANK ligand (RANKL) protein  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 15

ABR42314

ID ABR42314 standard; protein; 317 AA.

XX

AC ABR42314;

XX

DT 11-AUG-2003 (first entry)

XX

DE Human RANKL protein.

XX

KW Human; RANKL; tumour necrosis factor; ligand; cytostatic;

KW immunomodulator; osteopathic.

XX

OS Homo sapiens.

XX

PN WO2003040307-A2.

XX

PD 15-MAY-2003.

XX

PF 25-JUL-2002; 2002WO-US023782.

XX

PR 27-JUL-2001; 2001US-0307838P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Hilbert DH, Rosen CA;

XX

DR WPI; 2003-430659/40.

XX

PT New heteromultimeric complex having a first polypeptide member of the  
 PT tumor necrosis factor (TNF) ligand family, and a second different member  
 PT of TNF ligand family, useful for treating cancer, osteoporosis or an  
 PT autoimmune disease.

XX

PS Disclosure; Page 366-367; 388pp; English.

XX

CC The present sequence is the protein sequence of human RANKL protein. The  
 CC invention relates to compositions comprising heterotrimeric complexes of  
 CC tumour necrosis factor (TNF) ligand family members, and their use in the  
 CC detection, prevention and treatment of disease. In one embodiment, the

CC heterotrimeric complex comprises full-length or extracellular portions of  
CC RANKL and full-length or extracellular portions of other TNF ligand  
CC family members, preferably TRAIL. The heterotrimeric complexes of the  
CC invention are useful for treating an autoimmune disease, cancer or  
CC osteoporosis, and particularly for inhibiting cancer cell proliferation,  
CC increasing B cell proliferation, or inducing apoptosis of T cells. A  
CC claimed method of inhibiting cancer cell proliferation comprises  
CC administering a heterotrimeric complex consisting of TRAIL and CD40L or  
CC RANKL. A claimed method of treating osteoporosis comprises administering  
CC an antibody against a complex comprising RANKL and TRAIL  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
Best Local Similarity 100.0%; Pred. No. 6.2e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240
          |||
Db    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
          |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||
Db    301 PDQDATYFGAFKVRDID 317
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Search completed: November 8, 2004, 18:28:12  
Job time : 159 secs

OM protein - protein search, using sw model

Run on: November 8, 2004, 18:26:09 ; Search time 40 Seconds  
 (without alignments)  
 525.570 Million cell updates/sec

Title: US-09-787-126-2  
 Perfect score: 1685  
 Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1685	100.0	317	3	US-08-996-139-13	Sequence 13, Appl
2	1685	100.0	317	3	US-08-995-659-13	Sequence 13, Appl
3	1685	100.0	317	3	US-09-215-649A-13	Sequence 13, Appl
4	1685	100.0	317	3	US-09-052-521C-4	Sequence 4, Appli
5	1685	100.0	317	4	US-09-577-780-13	Sequence 13, Appl
6	1685	100.0	317	4	US-09-577-800-13	Sequence 13, Appl
7	1685	100.0	317	4	US-09-466-496-13	Sequence 13, Appl
8	1685	100.0	317	4	US-09-871-856-13	Sequence 13, Appl
9	1685	100.0	317	4	US-09-871-291-13	Sequence 13, Appl
10	1685	100.0	317	4	US-09-396-937-2	Sequence 2, Appli
11	1685	100.0	317	4	US-09-877-650-13	Sequence 13, Appl

12	1685	100.0	317	4	US-09-865-363-13	Sequence 13, Appl
13	1417.5	84.1	316	2	US-08-842-842-7	Sequence 7, Appli
14	1417.5	84.1	316	3	US-08-989-362-2	Sequence 2, Appli
15	1417.5	84.1	316	3	US-09-052-521C-2	Sequence 2, Appli
16	1417.5	84.1	316	4	US-09-671-658A-2	Sequence 2, Appli
17	1417.5	84.1	316	4	US-09-396-937-4	Sequence 4, Appli
18	1417.5	84.1	316	4	US-09-396-937-6	Sequence 6, Appli
19	1326.5	78.7	294	3	US-08-996-139-11	Sequence 11, Appl
20	1326.5	78.7	294	3	US-08-995-659-11	Sequence 11, Appl
21	1326.5	78.7	294	3	US-09-215-649A-11	Sequence 11, Appl
22	1326.5	78.7	294	4	US-09-577-780-11	Sequence 11, Appl
23	1326.5	78.7	294	4	US-09-577-800-11	Sequence 11, Appl
24	1326.5	78.7	294	4	US-09-466-496-11	Sequence 11, Appl
25	1326.5	78.7	294	4	US-09-871-856-11	Sequence 11, Appl
26	1326.5	78.7	294	4	US-09-871-291-11	Sequence 11, Appl
27	1326.5	78.7	294	4	US-09-877-650-11	Sequence 11, Appl
28	1326.5	78.7	294	4	US-09-865-363-11	Sequence 11, Appl
29	771	45.8	187	4	US-09-396-937-8	Sequence 8, Appli
30	769	45.6	173	4	US-09-396-937-10	Sequence 10, Appl
31	759	45.0	173	4	US-09-396-937-12	Sequence 12, Appl
32	721.5	42.8	188	4	US-09-396-937-14	Sequence 14, Appl
33	711.5	42.2	182	4	US-09-396-937-16	Sequence 16, Appl
34	691	41.0	173	4	US-09-396-937-18	Sequence 18, Appl
35	670	39.8	173	4	US-09-396-937-20	Sequence 20, Appl
36	418	24.8	77	4	US-09-632-287A-11	Sequence 11, Appl
37	363	21.5	77	4	US-09-632-287A-10	Sequence 10, Appl
38	251.5	14.9	279	3	US-09-072-993C-3	Sequence 3, Appli
39	251.5	14.9	281	1	US-08-670-354-2	Sequence 2, Appli
40	251.5	14.9	281	3	US-08-584-031-1	Sequence 1, Appli
41	251.5	14.9	281	3	US-08-780-496-1	Sequence 1, Appli
42	251.5	14.9	281	3	US-08-883-086-10	Sequence 10, Appl
43	251.5	14.9	281	3	US-09-320-424-2	Sequence 2, Appli
44	251.5	14.9	281	3	US-09-333-593A-6	Sequence 6, Appli
45	251.5	14.9	281	4	US-09-157-864-11	Sequence 11, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-996-139-13

; Sequence 13, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:



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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSSEHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300
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Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSSEHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy      301 PDQDATYFGAFKVRDID 317

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Db

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301 PDQDATYFGAFKVRDID 317

RESULT 2

US-08-995-659-13

; Sequence 13, Application US/08995659

; Patent No. 6242213

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/995,659

; FILING DATE: 22 DECEMBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-995-659-13

Query Match 100.0%; Score 1685; DB 3; Length 317;  
Best Local Similarity 100.0%; Pred. No. 3.7e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
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Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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RESULT 3

US-09-215-649A-13

; Sequence 13, Application US/09215649A

; Patent No. 6271349

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/215,649A

; FILING DATE: 17-Dec-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

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; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy     301 PDQDATYFGAFKVRDID 317
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Db     301 PDQDATYFGAFKVRDID 317

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RESULT 4
US-09-052-521C-4
; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors

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; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4
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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
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Db    181 KVSLSWYHDRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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# RESULT 5

US-09-577-780-13

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; Sequence 13, Application US/09577780
; Patent No. 6419929
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## GENERAL INFORMATION:

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; APPLICANT: Anderson, Dirk M.
;           Galibert, Laurent
;           Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Immunex Corporation, Law Department
;           STREET: 51 University Street
```

```

;      CITY: Seattle
;      STATE: WA
;      COUNTRY: USA
;      ZIP: 98101
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Power Macintosh
;      OPERATING SYSTEM: Apple Operating System 7.5.5
;      SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/577,780
;      FILING DATE: 24-May-2000
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/995,659
;      FILING DATE: <Unknown>
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2852-A
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPF AHLTINATDIPSGSH 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300

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Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
QY      301 PDQDATYFGAFKVRDID 317
      |||||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 6

US-09-577-800-13

; Sequence 13, Application US/09577800

; Patent No. 6479635

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/577,800

; FILING DATE: 24-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/996,139

; FILING DATE: 22 DECEMBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-577-800-13

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 3.7e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYL RGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYL RGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
|  
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
  
Qy 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
|  
Db 181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
|  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
  
Qy 301 PDQDATYFGAFKVRDID 317  
|  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 7

US-09-466-496-13

; Sequence 13, Application US/09466496

; Patent No. 6528482

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/466,496



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;      FILING DATE: 17-Dec-1999
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/996,139
;      FILING DATE: 22 DECEMBER 1997
;      APPLICATION NUMBER: USSN 60/064,671
;      FILING DATE: 14 OCTOBER 1997
;      APPLICATION NUMBER: USSN 08/813,509
;      FILING DATE: 07 MARCH 1997
;      APPLICATION NUMBER: USSN 08/772,330
;      FILING DATE: 23 DECEMBER 1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Perkins, Patricia Anne
;      REGISTRATION NUMBER: 34,693
;      REFERENCE/DOCKET NUMBER: 2851-A
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206)587-0430
;      TELEFAX: (206)233-0644
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 317 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-466-496-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 8



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Db          |||||
61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180
          |||||
Db          121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180

Qy          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMLV 240
          |||||
Db          181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMLV 240

Qy          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300
          |||||
Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD 300

Qy          301 PDQDATYFGAFKVRDID 317
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Db          301 PDQDATYFGAFKVRDID 317

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RESULT 9

US-09-871-291-13

; Sequence 13, Application US/09871291

; Patent No. 6562948

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLS SWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317

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RESULT 10

US-09-396-937-2

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; Sequence 2, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-396-937-2

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 3.7e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
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Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
| | | | |  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
| | | | |  
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
  
Qy 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
| | | | |  
Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
| | | | |  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
  
Qy 301 PDQDATYFGAFKVRDID 317  
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Db 301 PDQDATYFGAFKVRDID 317

RESULT 11

US-09-877-650-13

; Sequence 13, Application US/09877650  
; Patent No. 6649164

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

```

```

Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SSWYH DRGWAKISNM TFSNGKLIVNQDGFY YLYANICFRHHETSGDLATEYLQIMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLS SSWYH DRGWAKISNM TFSNGKLIVNQDGFY YLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12
US-09-865-363-13

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; Sequence 13, Application US/09865363
; Patent No. 6740522
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,363
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-865-363-13

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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.7e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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```

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
 Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 13

US-08-842-842-7

; Sequence 7, Application US/08842842

; Patent No. 5843678

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91230-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/842,842

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-451

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 316 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-842-842-7

Query Match 84.1%; Score 1417.5; DB 2; Length 316;

Best Local Similarity 84.3%; Pred. No. 6.6e-136;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;





; REGISTRATION NUMBER: 34,090  
 ; REFERENCE/DOCKET NUMBER: DX0686  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650)852-9196  
 ; TELEFAX: (650)496-1204  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 316 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-989-362-2

Query Match 84.1%; Score 1417.5; DB 3; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 6.6e-136;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59  
 ||||| ||| |||| ||| ||||| || ||| |||||:|||||  
 Db 1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60  
 Qy 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRR 119  
 |||:| ||||| ||||| ||| ||||| ||:|:| |||:|  
 Db 61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRR 118  
 Qy 120 KQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGS 179  
 ||||| ||||| ||| ||:|:|:|:| ||||| |||||  
 Db 119 KQAFQGA VQKELQHIVGPQR FSGAPAMMEG SWLDVAQRGKPEAQPFAH LTINAASIPSGS 178  
 Qy 180 HKVSLSSWYH DRGWAKISNM TFSNGK LIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239  
 ||:| ||||| ||||| ||||| ||||| ||||| ||||| :|:|  
 Db 179 HKVTLSSWYH DRGWAKISNM TFSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238  
 Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298  
 Qy 300 DPDQDATYFGAFKVRDID 317  
 ||||| ||||| |||||  
 Db 299 DPDQDATYFGAFKVQDID 316

RESULT 15  
 US-09-052-521C-2  
 ; Sequence 2, Application US/09052521C  
 ; Patent No. 6316408  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyle, William J.  
 ; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors  
 ; FILE REFERENCE: A-451Brv  
 ; CURRENT APPLICATION NUMBER: US/09/052,521C  
 ; CURRENT FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 08/880,855  
 ; PRIOR FILING DATE: 1997-06-23  
 ; PRIOR APPLICATION NUMBER: 08/842,842  
 ; PRIOR FILING DATE: 1997-04-16  
 ; NUMBER OF SEQ ID NOS: 40



OM protein - protein search, using sw model

Run on: November 8, 2004, 18:15:11 ; Search time 39 Seconds  
(without alignments)  
782.070 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	234	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	235	2	I54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	tumor necrosis fac
12	130.5	7.7	306	2	I49139	lymphotoxin-beta -
13	130	7.7	233	1	S22052	tumor necrosis fac

14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	CD40 ligand - mous
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta -
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	lymphotoxin alpha
25	92.5	5.5	450	2	S38114	hypothetical prote
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF3526	homoprotocatechuat
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A49733	[heparan sulfate]-
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHU7L	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

# ALIGNMENTS

## RESULT 1

I38707

Fas ligand - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

C;Accession: I38707; JC2340; S57565; I38554

R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A;Reference number: I38707; MUID:95127560; PMID:7826947

A;Accession: I38707

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-281 <RES>

A;Cross-references: UNIPROT:P48023; EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.;

Fusamoto, H.; Kamada, T.

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
 A;Reference number: JC2340; MUID:95071350; PMID:7980502  
 A;Accession: JC2340  
 A;Molecule type: DNA  
 A;Residues: 1-281 <MIT>  
 A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1;  
 PID:g1369902  
 R;Schatzlein, C.E.  
 submitted to the EMBL Data Library, June 1995  
 A;Reference number: S57565  
 A;Accession: S57565  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-281 <SCH>  
 A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456  
 R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley,  
 K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.  
 J. Exp. Med. 181, 71-77, 1995  
 A;Title: Fas ligand mediates activation-induced cell death in human T  
 lymphocytes.  
 A;Reference number: I38554; MUID:95105731; PMID:7528780  
 A;Accession: I38554  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-281 <RE2>  
 A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628  
 C;Genetics:  
 A;Gene: FasL  
 A;Introns: 151/1; 116/3  
 C;Keywords: glycoprotein; transmembrane protein  
 F;80-102/Domain: transmembrane #status predicted <TMM>  
 F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;  
 Best Local Similarity 21.7%; Pred. No. 2.2e-08;  
 Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

Qy	22	PGAPHEGPLHAPPPAP----	HQPPAASRS-----	MFVALLGLGLGQVVCS	63
				:    :	
Db	46	PPPPPPPLPPPPPPPLPPLPLPPLK	RGNHSTGLCLLMFFMVLVALVGLGLG-----		100
Qy	64	VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF			123
		:	: : :   :		
Db	101	--MFQLFHLQ-----	KELAELESTSQMHTA-----		124
Qy	124	QGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFALHT--INATDIPSGSHK			181
		: :   : :	:        : :		
Db	125	--SSLEKQIGH-----	PSPPPEKKELRKVAHLTGKSNRSRMP-----		159
Qy	182	VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMVY			241
		:   : :     : :     : : :	:		
Db	160	---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----		LPLSHK	210
Qy	242	VTKTSIKIPSSHTLMKGGSTKY-----	WSGNSEFHFYSINVGFFKLRSGEEISIEVSN		295
		:     :   :	:       : : :		
Db	211	VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----	YLGAVFNLTSAHLYVNVSE		263

QY 296 PSLLDPDQDATYFGAFKV 313  
 ||:: :: |:|| ::|:  
 Db 264 LSLVNFEESQTFFFGLYKL 281

# RESULT 2

A53062  
 Fas ligand - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: A53062  
 R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagata, S.  
 Cell 76, 969-976, 1994  
 A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.  
 A;Reference number: A53062; MUID:94185175; PMID:7511063  
 A;Accession: A53062  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-279 <TAK>  
 A;Cross-references: UNIPROT:P41047; GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.9%; Score 184.5; DB 2; Length 279;  
 Best Local Similarity 21.7%; Pred. No. 5.3e-08;  
 Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPLHAPPPAPHPQ-----PAASRSMFVALLGLGL 57  
 || :: | | || | | | | : |||:|:|  
 Db 38 RGPDQRRPPPPPPVSPPLPPPSQPLPLPLPTPLKKKDHTNLWLPPVFFMVLVALVGMGL 97  
 Qy 58 GQVVC SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
 | :|:: |  
 Db 98 G-----MYQLFHL----- 105  
 Qy 118 RIKQAFQGA VQKELQHI--VGSQHIRA---EKAMVDG SWLDLAKRSKLEAQPFAHLTINA 172  
 |||| : :| :: || : : | | : |||| |  
 Db 106 -----QKELAE LREFTNQSLKVSSF EKQIANPS----TPSEKKEPRSV AHLTGN- 150  
 Qy 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231  
 | : | | || : : | |::|: | |::|: : || :  
 Db 151 -----PHSR SIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN--- 201  
 Qy 232 ATEYLQ L MVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISI 291  
 : | ||: : | | ||: | : : :| : | | | : : :  
 Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGA VFNLT SADHLYV 257  
 Qy 292 EVSNPSLLDPDQDATYFGAFKV 313  
 :| ||:: :: |:|| ::|:  
 Db 258 NISQLSLINFEESKTFFGLYKL 279

# RESULT 3

S53090  
 CD40 ligand - bovine  
 C;Species: Bos primigenius taurus (cattle)

C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: S53090  
R;Mertens, B.E.L.C.; Muriuki, M.  
submitted to the EMBL Data Library, February 1995  
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.  
A;Reference number: S53090  
A;Accession: S53090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <MER>  
A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1;  
PID:g732570

Query Match 10.5%; Score 176.5; DB 2; Length 261;  
Best Local Similarity 24.2%; Pred. No. 2.3e-07;  
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

Qy	33	PPPPAPHQPPPAASRSMFVALLGLGL-GQVVCVSVALFFYFRAQMNDPNRISEDGTHCIYRIL	91
Db	8	PSPRSVATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R	57
Qy	92	RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRAEKAMVDG	149
Db	58	NLHEDFVFMKTIQRCNKGEGLSLLNCEEIERSRFEDLVKDIMGQ----NKEVKKKKEKNFE-	112
Qy	150	SWLDLAKRSKLEAQPFHAHLTINATDIPSGSHKVSLSWYHNRGWAKISN--MTFSNGK-L	206
Db	113	-----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYTSLNNLVTLENGKQL	161
Qy	207	IVNQDGFYYLYANICFRHHETSGDLATEYQLMVVYVTKTSIKIP--SSHTLMKGGSTKYW	264
Db	162	AVKRQGFYYIYTQVTFCSNR-----ETLSQAPFIASLCLKSPSGSERILLRAANTH--	212
Qy	265	SGNSEFHFYSINVGFFKLRSGEESISIEVSNPSLLDPDQDATYFGAFKV	313
Db	213	SSSKPCGQOOSIHLGGVFELOSGASVFVNVTDPSONVSHGTGFTSFGLLKL	261

## RESULT 4

A49266  
fas ligand - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A49266  
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.  
Cell 75, 1169-1178, 1993  
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of  
the tumor necrosis factor family.  
A;Reference number: A49266; MUID:94084792; PMID:7505205  
A;Accession: A49266  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-278 <SUD>  
A;Cross-references: UNIPROT:P36940; GB:U03470; NID:g440178; PIDN:AAC52129.1;  
PID:g440179  
C;Keywords: glycoprotein; transmembrane protein



Query Match 10.4%; Score 175.5; DB 2; Length 278;  
 Best Local Similarity 20.3%; Pred. No. 3e-07;  
 Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

```

Qy      21 GPGAPHEGPLHAPPPAPHPQPPAASRSM-----FVALLGLGL 57
      ||| | |||:| ||: : |||:|:|
Db      39 GPGQRRPPP--PPPPSPLPSPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96

Qy      58 GQVVCVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
      | : | | : : | | : | : : | | : : :
Db      97 G-----MYQLFHLQKELAEELREFTNHSI-RVSSFQKQIANPSTPSETKKPRSV----- 143

Qy     118 RIKQAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIPS 177
      ||| |
Db     144 -----AHLTG NPR----- 151

Qy     178 GSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
      | : | | | | : : | | : : | | : : : | : : |
Db     152 -SRSIPL-EWEDTYGTALISGVKYYKKGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205

Qy     238 L MVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPS 297
      ||: : | | ||: | : : | | | : : : | |
Db     206 HKVYM--RNFKYPGDLVLMEEKKLNCT-TGQIWAHSSYLGAVFNLTVDHLYVNISQLS 262

Qy     298 LLDPDQDATYFGAFKV 313
      |:: :: |::| ::
Db     263 LINFEESKTFFGLYKL 278

```

# RESULT 5

I53476

CD40 ligand - human

N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593

R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; Noelle, R.J.; Stamenkovic, I.; Ledbetter, J.A.; Aruffo, A. EMBO J. 11, 4313-4321, 1992

A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-stimulatory activity.

A;Reference number: S28017; MUID:93049181; PMID:1385114

A;Accession: S28017

A;Molecule type: mRNA

A;Residues: 1-261 <HOL>

A;Cross-references: UNIPROT:P29965; EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484

R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.A.; Maliszewski, C.R.; Fanslow, W.C. J. Exp. Med. 176, 1543-1550, 1992

A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.

A;Reference number: JH0793; MUID:93094757; PMID:1281209

A;Accession: JH0793

A;Molecule type: mRNA

A;Residues: 1-261 <SPR>  
 A;Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412  
 A;Experimental source: peripheral blood T-cell  
 R;Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; KroczeK, R.A.  
 Eur. J. Immunol. 22, 3191-3194, 1992  
 A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
 A;Reference number: S26694; MUID:93076854; PMID:1280226  
 A;Accession: S26694  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-261 <GRA>  
 A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270  
 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.;  
 Bonnefoy, J.Y.  
 FEBS Lett. 315, 259-266, 1993  
 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and  
 regulation of expression by factors controlling IgE production.  
 A;Reference number: S28852; MUID:93138085; PMID:7678552  
 A;Accession: S28852  
 A;Molecule type: mRNA  
 A;Residues: 1-261 <GAU>  
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124  
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having  
 6-Gln  
 C;Genetics:  
 A;Gene: GDB:CD40LG; HIGM1; IMD3  
 A;Cross-references: GDB:120632; OMIM:308230  
 A;Map position: Xq26-Xq26  
 C;Keywords: glycoprotein; transmembrane protein  
 F;13-44/Domain: transmembrane #status predicted <TMM>  
 F;45-261/Domain: extracellular #status predicted <EXT>  
 F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;  
 Best Local Similarity 24.5%; Pred. No. 7.7e-06;  
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

```

Qy      45 SRSMFVALLGLGL-GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDT- 102
      |  ::  || : |  |:: |      |  ::|  ::  ::      |||: | |
Db      20 SMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----RNLHEDFVFMKTI 69

Qy     103 -TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLE 161
      : : |  : |  ||  |:: |  ::      : | :  : | : :: | :
Db      70 QRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEETKKENSF-EMQKGDQ-N 119

Qy     162 AQPF AHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA 218
      | ||:  |:  |  | : |  ::|:  :|  |||  | | : | ||: ||
Db     120 PQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYA 173

Qy     219 NICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
      : | : : |  ::  :| |  |::  :|  |  ||:
Db     174 QVTFCSNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSAKPCGQQSIH 224

Qy     277 VGGFFKLRSGEESIEVSNPSLLDPDQDATYFGAFKV 313
      :|| |:: | : : |::|| :  | || | :
Db     225 LGGVFELQPGASVFVNVDPSQVSHGTGFTSFGLLKL 261
  
```

RESULT 6

QWMSN

tumor necrosis factor alpha precursor - mouse

N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004

C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.

DNA 7, 193-201, 1988

A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.

A;Reference number: A22908; MUID:88224564; PMID:2836146

A;Accession: A22908

A;Molecule type: DNA

A;Residues: 1-235 <SHI>

A;Cross-references: UNIPROT:P06804; GB:M20155

R;Shakhov, A.N.; Nedospasov, S.A.

Bioorg. Khim. 13, 701-705, 1987

A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence of the genomic copy of TNF-alpha in mice.

A;Reference number: S03791; MUID:87298639; PMID:3040015

A;Accession: S03791

A;Molecule type: DNA

A;Residues: 1-235 <SHA>

A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087

A;Note: article in Russian with English abstract

R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha- (tumor necrosis factor) and TNF-beta- (lymphotoxin) genes.

A;Reference number: A93679; MUID:88067722; PMID:3684584

A;Accession: A27303

A;Molecule type: DNA

A;Residues: 1-235 <SEM>

A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor.

A;Reference number: A25164; MUID:85298296; PMID:3898078

A;Accession: A25164

A;Molecule type: mRNA

A;Residues: 1-235 <PEN>

A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085

R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.;

Kawashima, E.; Chollet, A.; Tizard, R.; van Heuverswyn, H.; van Vliet, A.;

Ruysschaert, M.R.; Fiers, W.

Nucleic Acids Res. 13, 4417-4429, 1985

A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.

A;Reference number: A23127; MUID:85242112; PMID:2989794

A;Accession: A23127

A;Molecule type: mRNA

A;Residues: 1-235 <FRA>

A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R;Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989  
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted protein.  
A;Reference number: A34251; MUID:89380231; PMID:2777790  
A;Accession: A34251  
A;Molecule type: protein  
A;Residues: 70-87 <CSE>  
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A. Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of mRNA molecules specifying inflammatory mediators.  
A;Reference number: I59058; MUID:86149365; PMID:2419912  
A;Accession: I59058  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-230,'R',232-235 <RES>  
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083  
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A. Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor.  
A;Reference number: A36696; MUID:91097531; PMID:2268312  
A;Accession: A36696  
A;Molecule type: protein  
A;Residues: 80-85,'X',87-99 <SHE>  
C;Genetics:  
A;Introns: 62/3; 81/1; 97/1  
A;Note: the first intron occurs in the 5'-untranslated region  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
F;80-235/Product: tumor necrosis factor #status experimental <MAT>  
F;20/Binding site: myristate (Lys) (covalent) #status predicted  
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141.5; DB 1; Length 235;  
Best Local Similarity 25.9%; Pred. No. 0.00018;  
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVSL-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |          |:| | | | :|| | : :|| || | :|: :
Db      90 KPAHVVAN-----HQVEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLVSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:      |      :|: | |::      :|| |      :| | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCKDTPGAELKPW---- 192

Qy      269 EFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD-PDQDATYFG 309
          : | :|| |:| |::| ||: | || : |||
Db      193 ---YEPIYLGGVFQLEKGDQLSAEVLNLPKYLDFAESGQVYFG 231

```

RESULT 7  
A25451  
tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha  
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: A25454; A25451; JS0727  
 R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.; Kato, M.; Seko, M.  
 DNA 5, 149-156, 1986  
 A;Title: Molecular cloning and expression in *Escherichia coli* of the cDNA coding for rabbit tumor necrosis factor.  
 A;Reference number: A25454; MUID:86219711; PMID:3519137  
 A;Accession: A25454  
 A;Molecule type: mRNA  
 A;Residues: 1-234 <ITO>  
 A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760  
 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
 DNA 5, 157-165, 1986  
 A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
 A;Reference number: A25451; MUID:86219712; PMID:3519138  
 A;Accession: A25451  
 A;Molecule type: DNA  
 A;Residues: 1-234 <IT2>  
 A;Note: this sequence differs from that shown in having a Gln inserted between residues 62 and 63  
 R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
 Gene 95, 215-221, 1990  
 A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).  
 A;Reference number: JH0309; MUID:91065534; PMID:2249779  
 A;Accession: JS0727  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-62,'Q',63-234 <SHA>  
 A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756  
 C;Genetics:  
 A;Introns: 62/3; 80/1; 96/1  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
 F;1-81/Domain: propeptide #status predicted <PRO>  
 F;82-234/Product: tumor necrosis factor #status predicted <MAT>  
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;147-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;  
 Best Local Similarity 21.6%; Pred. No. 0.0002;  
 Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;

```
Qy      27  EGPLHAPPPAPHPQPPAASR----SMFVALLGLGLGQVVCSSVALFFYFRAQMDPNRISED 82
      |||| | : | |:| || | : | :|
Db      14  EGPL----PKKAGGPQGSKRCLCLSLFSFLLVAGATTLC----LLHFRVIGPQEEESPN 65

Qy      83  GTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQHIRA 142
      | : | | || |
```

```

Db      66 NLHLV-----NPVAQMVTLS-----A 82
Qy      143 EKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTF 201
      :|: |           :| ||: |   |   ::   |   |   | :| |
Db      83 SRALSD-----KPLAHVVAN-----PQVEGQL---QWLSQRANALLANGMKL 121
Qy      202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--- 258
      :: :|:| || | :|: : |   ||   | : |   | : : : : | :
Db      122 TDNQLVVPADGLYLIYSQVLF-----SGQGCRSYVLLTHTVSRFAVSYPNKNVLLSAIKS 176
Qy      259 -----GSTKYWSGNSEFHFYSINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYF 308
      |           : | :|| |:| | : :| ||: |   || :   ||
Db      177 PCHRETPEEAEPMAW-----YEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYF 229
Qy      309 G 309
      |
Db      230 G 230

```

# RESULT 8

JH0529

tumor necrosis factor alpha precursor - sheep

N;Alternate names: cachectin; TNF alpha

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: JH0529; S48118; S13114; S20661

R;Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.

A;Reference number: JH0529; MUID:92112044; PMID:1765267

A;Accession: JH0529

A;Molecule type: mRNA

A;Residues: 1-234 <GRE>

A;Cross-references: UNIPROT:P23383; EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A;Experimental source: alveolar macrophage

R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A;Reference number: S48118; MUID:92155784; PMID:1786996

A;Accession: S48118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-234 <NAS>

A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A;Reference number: S13114; MUID:91067496; PMID:2251151

A;Accession: S13114

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-62,64-234 <YOU>

A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A;Note: comparison with the introns of homologous sequences suggest that this is probably an alternative splicing

C;Superfamily: tumor necrosis factor  
 C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein;  
 lipoprotein; lymphokine; macrophage; myristylation; transmembrane protein  
 F;1-77/Domain: propeptide #status predicted <PRO>  
 F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
 F;20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;146-178/Disulfide bonds: #status predicted

Query Match 8.1%; Score 137; DB 1; Length 234;  
 Best Local Similarity 26.1%; Pred. No. 0.00043;  
 Matches 52; Conservative 30; Mismatches 71; Indels 46; Gaps 10;

```

QY      134 IVGSQHIRAEKAMVDGSW---LDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSW 187
      ::| | | |:: | | | | | | | | | | | | | | | | | | | | | | | |
Db      55 VIGPQ--REEQSPAGPSFNRPLVQTLRSSSQASNNKPVAVHVAN-----ISAP 100

QY      188 YHDRGWAKISNMFTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDL 231
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      101 GQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRI 160

QY      232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISI 291
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      161 AVSY-QTKVNIL-SAIKSPCHRETLEGAEAKPW-----YEPIYQGGVFQLEKGDRLSA 211

QY      292 EVSNPSLLD-PDQDATYFG 309
      |:: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      212 EINLPEYLDYAESGQVYFG 230
  
```

# RESULT 9

QWHUN

tumor necrosis factor alpha precursor [validated] - human

N;Alternate names: cachectin; TNFA

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 09-Jul-2004

C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522;  
 A01646; B23784

R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.;  
 Pennica, D.; Goeddel, D.V.; Gray, P.W.

Nucleic Acids Res. 13, 6361-6373, 1985

A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology  
 and chromosomal localization.

A;Reference number: A93585; MUID:86016093; PMID:2995927

A;Accession: A93585

A;Molecule type: DNA

A;Residues: 1-233 <NED>

A;Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209;  
 PIDN:CAA26669.1; PID:g37210

R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot,  
 V.; Jurka, J.; Rodriguez-Tome, P.; Claverie, J.M.; Dausset, J.; Cohen, D.  
 Nature Genet. 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the NFkappaB family  
 within a 90 kilobase HLA class III segment.

A;Reference number: S36152; MUID:93272029; PMID:8499947

A;Accession: S36153

A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-233 <IRI>  
 A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
 R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.; Kohr, W.J.; Aggarwal, B.B.; Goeddel, D.V.  
 Nature 312, 724-729, 1984  
 A;Title: Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin.  
 A;Reference number: A93351; MUID:85086244; PMID:6392892  
 A;Accession: A93351  
 A;Molecule type: mRNA  
 A;Residues: 1-233 <PEN>  
 A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
 A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelocytic leukemia  
 R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Yamamoto, R.; Mark, D.F.  
 Science 228, 149-154, 1985  
 A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
 A;Reference number: A44189; MUID:85142190; PMID:3856324  
 A;Accession: A44189  
 A;Molecule type: mRNA  
 A;Residues: 1-62,'S',64-233 <WAN>  
 A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738  
 R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.; Sugimoto, T.; Kurimoto, M.  
 Lymphokine Res. 7, 175-185, 1988  
 A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and interferon-alpha from BALL-1 cells stimulated by HVJ.  
 A;Reference number: A61478; MUID:88301617; PMID:2841543  
 A;Accession: B61478  
 A;Molecule type: protein  
 A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,'X',182-204 <FUK>  
 R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.  
 Eur. J. Biochem. 152, 515-522, 1985  
 A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison with mouse tumor nectosis factor.  
 A;Reference number: I53311; MUID:86030296; PMID:3932069  
 A;Accession: I53311  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-233 <MAR>  
 A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
 A;Experimental source: U-937 cells  
 R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
 Eur. J. Biochem. 235, 431-437, 1996  
 A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.  
 A;Reference number: S62610; MUID:96202967; PMID:8631363  
 A;Accession: S62610  
 A;Molecule type: protein



A;Residues: 77-99 <TAK>  
R;D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region.  
A;Reference number: I54522; MUID:94102809; PMID:7903959  
A;Accession: I54522  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-8 <DAL>  
A;Cross-references: GB:S68530; NID:g544751  
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues.  
A;Reference number: A59163; MUID:93018820; PMID:1402651  
A;Contents: annotation; identification of myristylated lysines  
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringman, T.S.; Nedwin, G.E.; Goeddel, D.V.; Harkins, R.N.  
J. Biol. Chem. 260, 2345-2354, 1985  
A;Title: Human tumor necrosis factor. Production, purification, and characterization.  
A;Reference number: A92511; MUID:85130974; PMID:3871770  
A;Contents: annotation; disulfide bond  
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction, TNF-alpha can cause cytolysis of certain tumor cell lines and have an antiproliferative effect on others without detriment to normal cells. It can also act synergistically with interferon gamma to kill certain transformed cell lines.  
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction kinetics.  
C;Genetics:  
A;Gene: GDB:TNF; TNFA  
A;Cross-references: GDB:120441; OMIM:191160  
A;Map position: 6p21.3-6p21.3  
A;Introns: 62/3; 78/1; 94/1  
C;Complex: homotrimer  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
F;1-76/Domain: propeptide #status predicted <PRO>  
F;77-233/Product: tumor necrosis factor #status experimental <MAT>  
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental  
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental  
F;145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;  
Best Local Similarity 25.5%; Pred. No. 0.00094;  
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221  
:| ||: | | : : | | : | : | : | : | :  
Db 87 KPAHVVAN----PQAEQQL---QWLNRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139  
Qy 222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273

```

      |:  :: || : : || :||| :| : || :
Db      140 FKGQGPCSTHVLTLTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGF FKLRS GEEISIEVSNPSLLD-PDQDATYFG 309
      | :|| |:| |: :| |: : | || :   |||
Db      193 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 229

```

# RESULT 10

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C;Species: Peromyscus leucopus (white-footed mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C;Accession: I54490

R;Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus (family Cricetidae).

A;Reference number: I54490; MUID:92218012; PMID:1348497

A;Accession: I54490

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-235 <RES>

A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C;Genetics:

A;Gene: PlTNF

A;Introns: 62/3; 81/1; 97/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

```

Query Match          7.9%;  Score 132.5;  DB 2;  Length 235;
Best Local Similarity 25.3%;  Pred. No. 0.0011;
Matches  42;  Conservative  27;  Mismatches  54;  Indels  43;  Gaps  7;

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```

Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMFTFSNG-----KLIVNQDGFYYL 216
      :| ||: |      |:| : || :|| :|| :||: ||| :
Db      90 KPAHVVAN-----HQVDEQLEWLSRG----ANALLANGMDLKDNLVIPADGLYLV 137

Qy      217 YANICFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYW 264
      |: : |: | : |: | |: : :||| :| ||
Db      138 YSQVLFK-----GQGCSSYVLLTHTVSRFAVSIEDKVNLLSAIKSPCPKETPEGSELKPW 192

Qy      265 SGNSEFHFYSINVGGF FKLRS GEEISIEVSNPSLLD-PDQDATYFG 309
      : | :|| |:| |: :| ||: | || :   |||
Db      193 -----YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

```

# RESULT 11

JU0029

tumor necrosis factor alpha precursor - rat

N;Alternate names: cachectin; TNF alpha

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004

C;Accession: JU0029; JN0868; S21674

R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.  
 Agric. Biol. Chem. 53, 1733-1736, 1989  
 A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.  
 A;Reference number: JU0029  
 A;Accession: JU0029  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SHI>  
 A;Cross-references: UNIPROT:P16599  
 R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.  
 Gene 132, 227-236, 1993  
 A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.  
 A;Reference number: JN0868; MUID:94040766; PMID:8224868  
 A;Accession: JN0868  
 A;Molecule type: DNA  
 A;Residues: 1-235 <KWO>  
 A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254  
 R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.  
 Biol. Chem. Hoppe-Seyler 373, 271-281, 1992  
 A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.  
 A;Reference number: S21674; MUID:92329007; PMID:1627266  
 A;Accession: S21674  
 A;Molecule type: mRNA  
 A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>  
 A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370  
 C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and produces hemorrhagic necrosis of tumors.  
 C;Genetics:  
 A;Gene: TNF-alpha  
 A;Introns: 62/3; 81/1; 97/1  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
 F;80-235/Product: tumor necrosis factor #status predicted <MAT>  
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;  
 Best Local Similarity 25.3%; Pred. No. 0.0013;  
 Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVSL-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |           |:           | | | :|| | : :||| || | :|: :
Db      90 KPAHVAVN-----HQAEQLEWLSQRANALLANGMDLKDNLVVPADGLYLIYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:           | :|: | |::           :||| | :| | |
Db      142 LFK-----QGCPDYVLLTHTVSRFAISYQEKVSLLSAISKSPCKDTPGAELKPW---- 192

Qy      269 EFHFYSINVGGFKLRSGEIEISIEVSNPSLLD-PDQDATYFG 309
          : : :|| |:| |: :| ||: | || :   |||
Db      193 ---YEPMYLGGVFQLEKGDLLSAEVLNPKYLDITESGQVYFG 231

```

RESULT 12

I49139

lymphotoxin-beta - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I49139; I49138; I49076

R;Lawton, P.; Nelson, J.; Tizard, R.; Browning, J.L.

J. Immunol. 154, 239-246, 1995

A;Title: Characterization of the mouse lymphotoxin-beta gene.

A;Reference number: I49138; MUID:95088371; PMID:7995944

A;Accession: I49139

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-306 <RES>

A;Cross-references: UNIPROT:P41155; EMBL:U16985; NID:g577830; PIDN:AAA70089.1; PID:g577831

A;Accession: I49138

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-306 <RE3>

A;Cross-references: EMBL:U16984; NID:g577431; PIDN:AAB60493.1; PID:g577432

R;Pokholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov,

S.V.; Novobrantseva, T.I.; Turetskaya, R.L.; Green, J.E.; Nedospasov, S.A.

Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995

A;Title: Cloning and expression analysis of the murine lymphotoxin beta gene.

A;Reference number: A55602; MUID:95148600; PMID:7846035

A;Accession: I49076

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-306 <RE2>

A;Cross-references: EMBL:U12029; NID:g515508; PIDN:AAA67716.1; PID:g515509

C;Genetics:

A;Gene: LT-beta

A;Introns: 54/3; 160/1

Query Match 7.7%; Score 130.5; DB 2; Length 306;

Best Local Similarity 22.1%; Pred. No. 0.0022;

Matches 55; Conservative 38; Mismatches 87; Indels 69; Gaps 12;

```

Qy      105 ESQDTKLIP---DSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLE 161
          | : | : | | : : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      86 ETPDPRLHPQRSNASRNLASTSQGPV-----AQSSREASAWMTI----- 124

Qy      162 AQPFAHLTIN--ATDIPSGSHKVSLS-----SWYHDRG--WAKISNMTF----- 201
          | | | : : | | : | : : | | : | | | | | | | | | | | | | | | | | | | | |
Db      125 LSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQ 184

Qy      202 ---SNGKLIVNQDGFYYLYANICFR--HHETSGDLATEYLQL--MVYVTKTSIKIPSSHTL 255
          : : | | : | | | | | | | : : | | : | | | | | | | | | | | | | | | | |
Db      185 FSPTHG-LALPQDGVYYLYCHVGYRGRTPPAGRSRARSILTLRSALYRAGGAYGRGSPELL 243

Qy      256 MKGGST-----KYWSGNSEFHFYSINVGGFKLRSGEESIEVSNPSLLDPDQD 304
          : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db      244 LEGAETVTPVVDPIGYGSLW-----YTSVGFGGLAQLRSGERVYVNISHPDMVDYRRG 296

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Qy 305 ATYFGAFKV 313  
|:| | | |  
Db 297 KTFFGAVMV 305

RESULT 13

S22052

tumor necrosis factor alpha precursor - baboon

C;Species: Papio sp. (baboon)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: S22052

R;Sanjanwala, M.; Edwards, A.

submitted to the EMBL Data Library, September 1991

A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A;Reference number: S22052

A;Accession: S22052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <SAN>

A;Cross-references: UNIPROT:P33620; EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C;Genetics:

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 7.7%; Score 130; DB 1; Length 233;  
Best Local Similarity 25.5%; Pred. No. 0.0017;  
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLIYANIC 221  
:| ||: | | :: | : | | ::| : : :|:| :| | :|: :  
Db 87 KPVAHVAN----PQAEQQL---QWLNRRANALLANGVELRDNLVVPSEGLYLIYSQVL 139  
  
Qy 222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEHFY 273  
|: : : | | : : | || :|| | :| | | :  
Db 140 FKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192  
  
Qy 274 SINVGGF FKLRS GEEISIEVSNPSLLD-PDQDATYFG 309  
| :|| |:| |: :| |: :| | | : |||  
Db 193 PIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229

RESULT 14

JQ1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: JQ1344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.  
A;Reference number: JQ1344; MUID:92084125; PMID:1748301  
A;Accession: JQ1344  
A;Molecule type: DNA  
A;Residues: 1-234 <SUX>  
A;Cross-references: UNIPROT:P29553; GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245  
C;Comment: This protein is an important proximal mediator of endotoxemia.  
C;Genetics:  
A;Gene: TNF-alpha  
A;Introns: 62/3; 79/1; 95/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;146-178/Disulfide bonds: #status predicted

Query Match 7.6%; Score 128; DB 1; Length 234;  
Best Local Similarity 24.2%; Pred. No. 0.0025;  
Matches 39; Conservative 32; Mismatches 58; Indels 32; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221  
:| ||: | | : : | | | :| : : :|:| || | :| :  
Db 88 KPVAHVVAN----PQAEQQL---QWLSGRANALLANGVKLTDNQLVVPLDGLYLIYSQVL 140  
Qy 222 FRHHETSGDLATEYQLQLMVYVTKTSIKIPSSHTLMKG-----GSTKYWSGNSE 269  
|: | :| | | : : :| | | : | |  
Db 141 FK---GQGCPTHVL-LTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPW----- 191  
Qy 270 FHFYSINVGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309  
: | :|| | :| | : :| | : : | | : |||  
Db 192 --YEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFG 230

# RESULT 15

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: UNIPROT:Q06599; EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor  
 C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F;20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;145-177/Disulfide bonds: #status predicted

Query Match 7.5%; Score 126.5; DB 1; Length 233;  
 Best Local Similarity 25.5%; Pred. No. 0.0033;  
 Matches 50; Conservative 25; Mismatches 80; Indels 41; Gaps 9;

```

Qy      134 IVGSQHIRAEKAMVDGSLDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSWYHD 190
          :| | :      | |  || :| :| ||:      || |
Db      55 VIGPQREESPGGPSINSPLVQTLRSSSQASSNKPVAHV---VADINSPGQL----- 102

Qy      191 RGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDLATE 234
          | | :| :||      :|:| || | :|: : ||      | :|
Db      103 RWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFRRGQCPSTPLFLTHTISRIAVS 162

Qy      235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVS 294
          | | | : :|| |      :      | |      : | || |:| |: :| |: :
Db      163 Y-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYQGGVFQLEKGDRLSAEIN 213

Qy      295 NPSLLD-PDQDATYFG 309
          | || :      |||
Db      214 LPDYLDYAESGQVYFG 229
  
```

Search completed: November 8, 2004, 18:28:56  
 Job time : 42 secs

OM protein - protein search, using sw model

Run on: November 8, 2004, 18:29:02 ; Search time 170 Seconds  
(without alignments)  
658.662 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES



Result No.	Score	Query Match	Length	DB	ID	Description
1	1685	100.0	317	9	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	9	US-09-871-856-13	Sequence 13, Appl
3	1685	100.0	317	9	US-09-957-944-6	Sequence 6, Appli
4	1685	100.0	317	9	US-09-865-363-13	Sequence 13, Appl
5	1685	100.0	317	9	US-09-871-291-13	Sequence 13, Appl
6	1685	100.0	317	9	US-09-877-650-13	Sequence 13, Appl
7	1685	100.0	317	14	US-10-151-071-10	Sequence 10, Appl
8	1685	100.0	317	14	US-10-218-547-22	Sequence 22, Appl
9	1685	100.0	317	14	US-10-405-878-13	Sequence 13, Appl
10	1685	100.0	317	14	US-10-167-182-11	Sequence 11, Appl
11	1685	100.0	317	14	US-10-310-793-28	Sequence 28, Appl
12	1685	100.0	317	14	US-10-460-623-11	Sequence 11, Appl
13	1685	100.0	317	15	US-10-289-456-79	Sequence 79, Appl
14	1685	100.0	317	15	US-10-202-062-22	Sequence 22, Appl
15	1685	100.0	317	16	US-10-664-801-2	Sequence 2, Appli
16	1685	100.0	317	16	US-10-381-160-6	Sequence 6, Appli
17	1685	100.0	317	17	US-10-799-345-12	Sequence 12, Appl
18	1424.5	84.5	316	9	US-09-957-944-8	Sequence 8, Appli
19	1424.5	84.5	316	17	US-10-799-345-10	Sequence 10, Appl
20	1422	84.4	270	15	US-10-289-456-80	Sequence 80, Appl
21	1417.5	84.1	316	10	US-09-079-569-7	Sequence 7, Appli
22	1417.5	84.1	316	10	US-09-873-829-4	Sequence 4, Appli
23	1417.5	84.1	316	13	US-10-017-910-4	Sequence 4, Appli
24	1417.5	84.1	316	14	US-10-105-057-2	Sequence 2, Appli
25	1417.5	84.1	316	14	US-10-272-411-19	Sequence 19, Appl
26	1417.5	84.1	316	14	US-10-272-328A-19	Sequence 19, Appl
27	1417.5	84.1	316	14	US-10-326-052-2	Sequence 2, Appli
28	1417.5	84.1	316	14	US-10-167-182-1	Sequence 1, Appli
29	1417.5	84.1	316	14	US-10-460-623-1	Sequence 1, Appli
30	1417.5	84.1	316	16	US-10-664-801-4	Sequence 4, Appli
31	1417.5	84.1	316	16	US-10-664-801-6	Sequence 6, Appli
32	1326.5	78.7	294	9	US-09-871-856-11	Sequence 11, Appl
33	1326.5	78.7	294	9	US-09-865-363-11	Sequence 11, Appl
34	1326.5	78.7	294	9	US-09-871-291-11	Sequence 11, Appl
35	1326.5	78.7	294	9	US-09-877-650-11	Sequence 11, Appl
36	1326.5	78.7	294	14	US-10-405-878-11	Sequence 11, Appl
37	1325	78.6	250	14	US-10-338-785A-1	Sequence 1, Appli
38	1325	78.6	250	16	US-10-611-363-1	Sequence 1, Appli
39	1319	78.3	249	14	US-10-050-902-221	Sequence 221, App
40	1319	78.3	249	14	US-10-050-898-221	Sequence 221, App
41	1319	78.3	249	15	US-10-289-456-82	Sequence 82, Appl
42	1301	77.2	246	14	US-10-167-182-17	Sequence 17, Appl
43	1301	77.2	246	14	US-10-460-623-17	Sequence 17, Appl
44	1293	76.7	245	10	US-09-873-829-2	Sequence 2, Appli
45	1293	76.7	245	13	US-10-017-910-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
 US-09-813-329-7  
 ; Sequence 7, Application US/09813329  
 ; Patent No. US20020012968A1

```
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor
Class Molecule ("DmTNF") and
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7
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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
      |||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
      |||
Db    181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
      |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      |||
Db    301 PDQDATYFGAFKVRDID 317
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# RESULT 2

US-09-871-856-13

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; Sequence 13, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/871,856  
FILING DATE: 31-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,139  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2851-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

[illegible]

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Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        |||
Db      301 PDQDATYFGAFKVRDID 317

```

RESULT 3

US-09-957-944-6

; Sequence 6, Application US/09957944

; Publication No. US20020086312A1

; GENERAL INFORMATION:

; APPLICANT: Dougall, William C.

; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVATOR OF

; TITLE OF INVENTION: NF-kappa B

; FILE REFERENCE: 3109-A

; CURRENT APPLICATION NUMBER: US/09/957,944

; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/235,157

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 317

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-957-944-6

Query Match 100.0%; Score 1685; DB 9; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
        |||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
Qy      121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        |||
Db      121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSSLLD 300
        |||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSSLLD 300

```

Qy 301 PDQDATYFGAFKVRDID 317  
| | | | | | | | | | | | | | | |  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 4

US-09-865-363-13

; Sequence 13, Application US/09865363

; Publication No. US20020086826A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/865,363

; FILING DATE: 25-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-865-363-13

Query Match 100.0%; Score 1685; DB 9; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180

QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

QY 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

US-09-871-291-13

; Sequence 13, Application US/09871291

; Publication No. US20020086827A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

```

; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13

```

```

Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

```

RESULT 6

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. US20020169117A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

```

```

Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQLMV 240
        |||

```



```

Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 7

US-10-151-071-10

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; Sequence 10, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-10

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Query Match          100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Qy      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Qy      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
Qy      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Qy      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy      301 PDQDATYFGAFKVRDID 317

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Db 301 PDQDATYFGAFKVRDID 317

RESULT 8  
US-10-218-547-22  
; Sequence 22, Application US/10218547  
; Publication No. US20030100074A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relating To  
; TITLE OF INVENTION: Human Endokine Alpha  
; FILE REFERENCE: PF561  
; CURRENT APPLICATION NUMBER: US/10/218,547  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/312,542  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/330,761  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: human  
US-10-218-547-22

Query Match 100.0%; Score 1685; DB 14; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.5e-149;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAH LTINATDIPSGSH 180  
|  
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPFAH LTINATDIPSGSH 180  
  
Qy 181 KVSLS SWYH DRGWAKISNMTFSNGKLI VNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
|  
Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLI VNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
  
Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNP SLLD 300  
|  
Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNP SLLD 300  
  
Qy 301 PDQDATYFGAFKVRDID 317  
|  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 9

US-10-405-878-13

; Sequence 13, Application US/10405878

; Publication No. US20030175840A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/405,878

; FILING DATE: 01-Apr-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 22 DECEMBER 1997

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-405-878-13

Query Match 100.0%; Score 1685; DB 14; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
 |||

Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||

Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180  
 |||

Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFHAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 |||

Db 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
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Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 10

US-10-167-182-11

; Sequence 11, Application US/10167182

; Publication No. US20030176647A1

; GENERAL INFORMATION:

; APPLICANT: Yamaguchi, Kyoji

; APPLICANT: Yasuda, Hisataka

; APPLICANT: Nakagawa, No. US20030176647Aluaki

; APPLICANT: Shima, No. US20030176647Aluyuki

; APPLICANT: Kinosaki, Masahiko

; APPLICANT: Tsuda, Eisuke

; APPLICANT: Goto, Masaaki

; APPLICANT: Yano, Kazuki

; APPLICANT: Tomoyasu, Akihiro

; APPLICANT: Kobayashi, Fumie

; APPLICANT: Washida, Naohiro

; APPLICANT: Takahashi, Ken

; APPLICANT: Morinaga, Tomonori

; APPLICANT: Higashio, Kanji

; TITLE OF INVENTION: Antibodies to OCIF-binding Molecules

; FILE REFERENCE: FJN-070DV

; CURRENT APPLICATION NUMBER: US/10/167,182

; CURRENT FILING DATE: 2002-06-11

; PRIOR APPLICATION NUMBER: US 09/202,455

; PRIOR FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: JP 97808/1997

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: JP 151434/1997

; PRIOR FILING DATE: 1997-06-09

; PRIOR APPLICATION NUMBER: JP 217897/1997

; PRIOR FILING DATE: 1997-08-12

; PRIOR APPLICATION NUMBER: JP 224803/1997

; PRIOR FILING DATE: 1997-08-21

; PRIOR APPLICATION NUMBER: JP 332241/1997

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; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-167-182-11
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Query Match 100.0%; Score 1685; DB 14; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.5e-149;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTF SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTF SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

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RESULT 11
US-10-310-793-28
; Sequence 28, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel
Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695

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; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: human
US-10-310-793-28

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Query Match          100.0%;   Score 1685;   DB 14;   Length 317;
Best Local Similarity 100.0%;   Pred. No. 2.5e-149;
Matches 317;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPPFAHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPPFAHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12  
 US-10-460-623-11  
 ; Sequence 11, Application US/10460623  
 ; Publication No. US20030208045A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yamaguchi, Kyoji  
 ; APPLICANT: Yasuda, Hisataka  
 ; APPLICANT: Nakagawa, No. US20030208045Aluaki  
 ; APPLICANT: Shima, No. US20030208045Aluyuki  
 ; APPLICANT: Kinosaki, Masahiko  
 ; APPLICANT: Tsuda, Eisuke  
 ; APPLICANT: Goto, Masaaki  
 ; APPLICANT: Yano, Kazuki  
 ; APPLICANT: Tomoyasu, Akihiro  
 ; APPLICANT: Kobayashi, Fumie  
 ; APPLICANT: Washida, Naohiro  
 ; APPLICANT: Takahashi, Ken  
 ; APPLICANT: Morinaga, Tomonori  
 ; APPLICANT: Higashio, Kanji  
 ; TITLE OF INVENTION: No. US20030208045A1el Protein and Method for Producing  
 the Protein  
 ; FILE REFERENCE: FJN-070  
 ; CURRENT APPLICATION NUMBER: US/10/460,623  
 ; CURRENT FILING DATE: 2003-06-13  
 ; PRIOR APPLICATION NUMBER: JP 97808/1997  
 ; PRIOR FILING DATE: 1997-04-15  
 ; PRIOR APPLICATION NUMBER: JP 151434/1997  
 ; PRIOR FILING DATE: 1997-06-09  
 ; PRIOR APPLICATION NUMBER: JP 217897/1997  
 ; PRIOR FILING DATE: 1997-08-12  
 ; PRIOR APPLICATION NUMBER: JP 224803/1997  
 ; PRIOR FILING DATE: 1997-08-21  
 ; PRIOR APPLICATION NUMBER: JP 332241/1997  
 ; PRIOR FILING DATE: 1997-12-02  
 ; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 317  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-460-623-11

Query Match 100.0%; Score 1685; DB 14; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-149;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAQVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAPHLTINATDIPSGSH	180

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Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
QY      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
QY      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
QY      301 PDQDATYFGAFKVRDID 317
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 13

US-10-289-456-79

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; Sequence 79, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-289-456-79

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Query Match          100.0%; Score 1685; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
QY      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
QY      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

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Db      121  |||||
QY      181  KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
Db      181  |||||
QY      241  YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Db      241  |||||
QY      301  PDQDATYFGAFKVRDID 317
Db      301  |||||
Db      301  PDQDATYFGAFKVRDID 317

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RESULT 14

US-10-202-062-22

; Sequence 22, Application US/10202062

; Publication No. US20040038349A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.,

; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members

; FILE REFERENCE: PF559

; CURRENT APPLICATION NUMBER: US/10/202,062

; CURRENT FILING DATE: 2002-07-25

; PRIOR APPLICATION NUMBER: 60/307,838

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-202-062-22

Query Match 100.0%; Score 1685; DB 15; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-149;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
Db      1  MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY      61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
Db      61  VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180
Db      121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAH LTINATDIPSGSH 180

QY      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

QY      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

```

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Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEIEISIEVSNPSLLD 300
QY      301 PDQDATYFGAFKVRDID 317
          |||||
Db      301 PDQDATYFGAFKVRDID 317

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RESULT 15

US-10-664-801-2

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; Sequence 2, Application US/10664801
; Publication No. US20040115199A1
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/10/664,801
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/396,937
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-801-2

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Query Match          100.0%; Score 1685; DB 16; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-149;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
          |||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

QY      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||||
Db      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

QY      121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
          |||||
Db      121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

QY      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240
          |||||
Db      181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

QY      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEIEISIEVSNPSLLD 300
          |||||
Db      241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFCKLRSGEIEISIEVSNPSLLD 300

QY      301 PDQDATYFGAFKVRDID 317
          |||||

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Db

301 PDQDATYFGAFKVRDID 317

Search completed: November 8, 2004, 18:44:23

Job time : 173 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 18:23:14 ; Search time 192 Seconds  
(without alignments)  
949.968 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	1	TN11_HUMAN	O14788 h tumor nec
2	1417.5	84.1	316	1	TN11_MOUSE	O35235 m tumor nec
3	1396.5	82.9	318	1	TN11_RAT	Q9ese2 r tumor nec
4	1292	76.7	244	2	BAB79693	Bab79693 homo sapi
5	266	15.8	317	2	Q7ZYX9	Q7zyx9 brachydanio
6	265	15.7	304	2	Q7T1F2	Q7t1f2 gallus gall
7	251.5	14.9	281	1	TN10_HUMAN	P50591 homo sapien
8	251.5	14.9	281	2	CAG33176	Cag33176 homo sapi
9	249.5	14.8	299	2	Q6DHG9	Q6dhg9 brachydanio
10	248	14.7	291	1	TN10_MOUSE	P50592 mus musculu
11	240.5	14.3	214	2	Q9DDZ5	Q9ddz5 brachydanio
12	216.5	12.8	287	2	Q90WT9	Q90wt9 gallus gall
13	215.5	12.8	287	2	Q8K3G0	Q8k3g0 rattus norv
14	200	11.9	282	1	TNF6_PIG	Q9bea8 sus scrofa
15	194.5	11.5	280	2	Q861W5	Q861w5 felis silve

16	189	11.2	281	1	TNF6_HUMAN	P48023 homo sapien
17	189	11.2	281	2	AAO43991	Aao43991 homo sapi
18	187.5	11.1	279	2	Q7TMV9	Q7tmv9 mus musculu
19	186	11.0	280	1	TNF6_MACMU	Q9myl6 macaca mula
20	184.5	10.9	252	2	Q8K3Y8	Q8k3y8 mus musculu
21	184.5	10.9	279	1	TNF6_MOUSE	P41047 mus musculu
22	184.5	10.9	279	2	BAC30520	Bac30520 mus muscu
23	182.5	10.8	280	1	TNF6_CERTO	Q9bdn1 cercocebus
24	181	10.7	95	2	Q6UWL7	Q6uwl7 homo sapien
25	181	10.7	95	2	Q6UY13	Q6uy13 homo sapien
26	181	10.7	95	2	AAQ88490	Aaq88490 homo sapi
27	181	10.7	95	2	AAQ89101	Aaq89101 homo sapi
28	179.5	10.7	252	2	Q80YZ0	Q80yz0 mus musculu
29	177.5	10.5	252	2	Q8K3Y7	Q8k3y7 rattus norv
30	176.5	10.5	261	1	TNF5_BOVIN	P51749 bos taurus
31	175.5	10.4	278	1	TNF6_RAT	P36940 rattus norv
32	169.5	10.1	261	1	TNF5_CALJA	Q9bdn3 callithrix
33	167.5	9.9	261	1	TNF5_AOTTR	Q9bdm3 aotus trivi
34	158.5	9.4	261	1	TNF5_HUMAN	P29965 homo sapien
35	158.5	9.4	261	2	AAH71754	Aah71754 homo sapi
36	156.5	9.3	251	2	Q8NFE9	Q8nfe9 homo sapien
37	156.5	9.3	251	2	AAH69435	Aah69435 homo sapi
38	155.5	9.2	261	1	TNF5_MACMU	Q9bdc7 macaca mula
39	155	9.2	272	1	TNF5_CHICK	Q9i8d8 gallus gall
40	152.5	9.1	261	1	TNF5_PIG	Q95mq5 sus scrofa
41	152	9.0	260	1	TNF5_FELCA	O97605 felis silve
42	146	8.7	234	1	TNFA_CAVPO	P51435 cavia porce
43	145.5	8.6	239	1	TN14_MOUSE	Q9qyh9 mus musculu
44	145	8.6	174	1	TN15_HUMAN	O95150 homo sapien
45	145	8.6	260	1	TNF5_CANFA	O97626 canis famil

# ALIGNMENTS

## RESULT 1

### TN11\_HUMAN

ID TN11\_HUMAN STANDARD; PRT; 317 AA.

AC O14788; O14723; Q96Q17; Q9P2Q3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
DE differentiation factor) (ODF).

GN Name=TNFSF11; Synonyms=RANKL, TRANCE, OPGL;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Bone marrow, and Peripheral blood;

RX MEDLINE=98032977; PubMed=9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,

RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,

RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function."  
 RL Nature 390:175-179(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Lymph node;  
 RX MEDLINE=98227661; PubMed=9568710;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation."  
 RL Cell 93:165-176(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RA Ikeda T., Kuroyama H., Hirokawa K.;  
 RT "Determination of human RANKL isoforms."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE OF 73-317 FROM N.A.  
 RC TISSUE=Thymocytes;  
 RX MEDLINE=97460112; PubMed=9312132;  
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,  
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells."  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Tongue;  
 RX MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;  
 RA Nagai M., Kyakumoto S., Sato N.;  
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA  
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast  
 RT formation."  
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);  
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by  
 CC proteolytic processing (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O14788-1; Sequence=Displayed;  
 CC Name=2; Synonyms=SODF;

```

CC      IsoId=014788-2; Sequence=VSP_006447;
CC      Name=3;
CC      IsoId=014788-3; Sequence=VSP_006446;
CC      -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC          spleen, peripheral blood Leukocytes, bone marrow, heart, placenta,
CC          skeletal muscle, stomach and thyroid.
CC      -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC      -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC          by proteolytic processing (By similarity). The cleavage may be
CC          catalyzed by ADAM17.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019047; AAB86811.1; -.
DR      EMBL; AF053712; AAC39731.1; -.
DR      EMBL; AB064269; BAB79694.1; -.
DR      EMBL; AB061227; BAB71768.1; -.
DR      EMBL; AB064270; BAB79695.1; -.
DR      EMBL; AF013171; AAC51762.1; -.
DR      EMBL; AB037599; BAA90488.1; -.
DR      HSSP; O35235; 1JTZ.
DR      Genew; HGNC:11926; TNFSF11.
DR      MIM; 602642; -.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0005887; C:integral to plasma membrane; NAS.
DR      GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      GO; GO:0030316; P:osteoclast differentiation; NAS.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Alternative splicing; Cytokine; Differentiation; Glycoprotein;
KW      Receptor; Signal-anchor; Transmembrane.
FT      CHAIN      1      317      Tumor necrosis factor ligand superfamily
FT                                     member 11, membrane form.
FT      CHAIN      140     317      Tumor necrosis factor ligand superfamily
FT                                     member 11, soluble form (By similarity).
FT      DOMAIN      1      47      Cytoplasmic (Potential).
FT      TRANSMEM     48     68      Signal-anchor for type II membrane
FT                                     protein (Potential).
FT      DOMAIN      69     317      Extracellular (Potential).
FT      SITE       139     140      Cleavage (By similarity).
FT      CARBOHYD    171     171      N-linked (GlcNAc . . .) (Potential).
FT      CARBOHYD    198     198      N-linked (GlcNAc . . .) (Potential).
FT      VARSPLIC     1      47      Missing (in isoform 3).

```

FT /FTid=VSP\_006446.  
 FT VARSPLIC 1 73 Missing (in isoform 2).  
 FT /FTid=VSP\_006447.  
 FT CONFLICT 194 194 A -> G (in Ref. 4).  
 SQ SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;

Query Match 100.0%; Score 1685; DB 1; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-134;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
 QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
 QY 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
  
 QY 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLS SWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240  
  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLLD 300  
  
 QY 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

## RESULT 2

### TN11\_MOUSE

ID TN11\_MOUSE STANDARD; PRT; 316 AA.  
 AC O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)  
 DE (OCIF).  
 GN Name=Tnfsf11; Synonyms=RANKL, Trance, OPGL;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Hybridoma;  
 RX MEDLINE=97460112; PubMed=9312132;  
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,



RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.";  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thymic lymphoma;  
 RX MEDLINE=98032977; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98227661; PubMed=9568710;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation.";  
 RL Cell 93:165-176(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow stroma;  
 RX MEDLINE=98188248; PubMed=9520411;  
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,  
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,  
 RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
 RT "Osteoclast differentiation factor is a ligand for  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
 RT to TRANCE/RANKL.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=129;  
 RX MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;  
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
 RA Ueda M., Higashio K.;  
 RT "Cloning and characterization of the gene encoding mouse osteoclast  
 RT differentiation factor.";  
 RL Gene 230:121-127(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=21150053; PubMed=11250921;  
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
 RT "Determination of three isoforms of the receptor activator of nuclear  
 RT factor-kappaB ligand and their differential expression in bone and  
 RT thymus.";  
 RL Endocrinology 142:1419-1426(2001).  
 RN [7]  
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.

RX MEDLINE=99240759; PubMed=10224132;  
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,  
 RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;  
 RT "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-  
 RT converting enzyme-like protease in shedding of TRANCE, a TNF family  
 RT member involved in osteoclastogenesis and dendritic cell survival.";  
 RL J. Biol. Chem. 274:13613-13618(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
 RX MEDLINE=21464816; PubMed=11581298;  
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
 RT of receptor-ligand specificity.";  
 RL J. Clin. Invest. 108:971-979(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
 RX MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;  
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 RT 2.2-A resolution.";  
 RL J. Biol. Chem. 277:6631-6636(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O35235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O35235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=O35235-3; Sequence=VSP\_006448;  
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,  
 CC but not in nonlymphoid tissues and is abundantly expressed in T  
 CC cells but not in B cells. A high level expression is also seen in  
 CC the trabecular bone and lung.  
 CC -!- PTM: N-glycosylated.  
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-  
 CC alveolar mammary structures during pregnancy, resulting in death  
 CC of newborns. Trance-deficient mice show severe osteopetrosis, with  
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit  
 CC profound growth retardation at several skeletal sites, including  
 CC the limbs, skull, and vertebrae and have marked chondrodysplasia,  
 CC with thick, irregular growth plates and a relative increase in  
 CC hypertrophic chondrocytes.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

```

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CC -----
DR EMBL; AF013170; AAC71061.1; -.
DR EMBL; AF019048; AAB86812.1; -.
DR EMBL; AF053713; AAC40113.1; -.
DR EMBL; AB008426; BAA25425.1; -.
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR EMBL; AB032771; BAA97257.1; -.
DR EMBL; AB032772; BAA97258.1; -.
DR EMBL; AB036798; BAA97259.1; -.
DR PDB; 1IQA; X-ray; A/B/C=157-316.
DR PDB; 1JTZ; X-ray; X/Y/Z=146-316.
DR MGD; MGI:1100089; Tnfsf11.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042804; F:protein homooligomerization activity; IDA.
DR GO; GO:0045453; P:bone resorption; IDA.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0001503; P:ossification; IMP.
DR GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW 3D-structure; Alternative splicing; Cytokine; Differentiation;
KW Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;
KW Transmembrane.
FT CHAIN 1 316 Tumor necrosis factor ligand superfamily
FT member 11, membrane form.
FT CHAIN 139 316 Tumor necrosis factor ligand superfamily
FT member 11, soluble form.
FT DOMAIN 1 48 Cytoplasmic (Potential).
FT TRANSMEM 49 69 Signal-anchor for type II membrane
FT protein (Potential).
FT DOMAIN 70 316 Extracellular (Potential).
FT SITE 138 139 Cleavage.
FT CARBOHYD 197 197 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 262 262 N-linked (GlcNAc . . .) (Potential).
FT VARSPLIC 1 117 Missing (in isoform 3).
FT /FTId=VSP_006448.
FT VARSPLIC 14 44 SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in
FT isoform 2).
FT /FTId=VSP_006449.
FT CONFLICT 99 99 G -> D (in Ref. 2).

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FT	CONFLICT	141	143	Missing (in Ref. 5).
FT	STRAND	164	169	
FT	TURN	171	172	
FT	STRAND	181	182	
FT	STRAND	186	187	
FT	TURN	191	192	
FT	STRAND	194	196	
FT	STRAND	198	201	
FT	TURN	202	203	

Query Match 84.1%; Score 1417.5; DB 1; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 6.1e-112;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQ	59
		:	
Db	1	MRRASRDYGKYLRSEEMGSGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ	60
Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI	119
		:                                 :    :     :      :	
Db	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM	118
Qy	120	KQAFQGA VQKELQHIVG SQHIRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGS	179
		:      :	
Db	119	KQAFQGA VQKELQHIVG PQRFS GAPAMMEG SWLDVAQRGKPEAQPF AHLTINAASIPSGS	178
Qy	180	HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
		:   :   :	
Db	179	HKVTLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSVPTDYLQLM	238
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL	299
		:      :	
Db	239	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL	298
Qy	300	DPDQDATYFGAFKVRDID	317
Db	299	DPDQDATYFGAFKVQDID	316

# RESULT 3

## TN11\_RAT

ID TN11\_RAT STANDARD; PRT; 318 AA.  
 AC Q9ESE2; Q91ZI9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
 DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
 DE differentiation factor) (ODF).  
 GN Name=Tnfsf11; Synonyms=RANKL, Trance, Opgl;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Tibial bone;  
 RX MEDLINE=20540945; PubMed=11092398;  
 RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,  
 RA Zheng M.H.;  
 RT "Cloning, sequence and functional characterization of the rat  
 RT homologue of receptor activator of NF-kB ligand.";  
 RL J. Bone Miner. Res. 15:2178-2186(2000).  
 RN [2]  
 RP SEQUENCE OF 266-318 FROM N.A.  
 RC STRAIN=Fischer 344;  
 RX MEDLINE=21662371; PubMed=11804028;  
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,  
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,  
 RA Marks S.C. Jr.;  
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in  
 RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";  
 RL Int. J. Dev. Biol. 45:853-859(2001).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF187319; AAG17031.1; -.  
 DR EMBL; AF425669; AAL23963.1; -.  
 DR HSSP; O35235; 1JTZ.  
 DR RGD; 620784; Tnfsf11.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Differentiation; Glycoprotein; Receptor; Signal-anchor;  
 KW Transmembrane.  
 FT CHAIN 1 318 Tumor necrosis factor ligand superfamily  
 FT member 11, membrane form.

FT CHAIN 141 318 Tumor necrosis factor ligand superfamily  
 FT member 11, soluble form.  
 FT DOMAIN 1 47 Cytoplasmic (Potential).  
 FT TRANSMEM 48 68 Signal-anchor for type II membrane  
 FT protein (Potential).  
 FT DOMAIN 69 318 Extracellular (Potential).  
 FT SITE 140 141 Cleavage (By similarity).  
 FT CARBOHYD 199 199 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 264 264 N-linked (GlcNAc. . .) (Potential).  
 FT CONFLICT 317 317 I -> M (in Ref. 2).  
 SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 82.9%; Score 1396.5; DB 1; Length 318;  
 Best Local Similarity 82.4%; Pred. No. 3.8e-110;  
 Matches 262; Conservative 19; Mismatches 36; Indels 1; Gaps 1;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59  
 ||||:||||| ||||| || ||||| || ||| ||||| ||:|||||  
 Db 1 MRRANRDYGKYLRGSEEMGSCPGVPHEGPLHPAPSAPAPAPPPAASRFMFLALLGLGLGQ 60  
 Qy 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119  
 ||||:||||| ||||| ||||| || ||||| || ||:||||:||||: |||||:  
 Db 61 VVCSIALFLYFRAQMDPNRISEDSRCFYRILRLRENTGLQDSTLESEDTEALPDSCRRM 120  
 Qy 120 KQAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGS 179  
 |||||:||||| | ||::|||:|:| | ||||| |||||  
 Db 121 KQAFQGA VQRELQHIVGPQRFSGVPAMMEGSWLDVARRGKPEAQPF AHLTINAADIPSGS 180  
 Qy 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| : : |||||  
 Db 181 HKVSLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPADYLQLM 240  
 Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299  
 ||| ||||| ||||| ||||| ||||| ||||| |||||:||||:|||||  
 Db 241 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKL RAGEEISVQVSNPSLL 300  
 Qy 300 DPDQDATYFGAFKVRDID 317  
 ||||| |||||:||||  
 Db 301 DPDQDATYFGAFKVQDID 318

#### RESULT 4 BAB79693

ID BAB79693 PRELIMINARY; PRT; 244 AA.  
 AC BAB79693;  
 DT 24-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 24-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 24-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Receptor activator of nuclear factor kappa B ligand 3.  
 GN HRANKL 3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Utsuyama M.,

RA Tatsumi M., Uematsu H., Hirokawa K.;  
 RT "Regulation of osteoclastogenesis by three human RANKL isoforms  
 RT expressed in NIH3T3 cells.";  
 RL Biochem. Biophys. Res. Commun. 314:1021-1027(2004).  
 DR EMBL; AB064268; BAB79693.1; -.  
 KW Receptor.  
 SQ SEQUENCE 244 AA; 27690 MW; C827590684B6B83C CRC64;

Query Match 76.7%; Score 1292; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 2e-101;  
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 MDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQH 133  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQH 60

QY 134 IVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDRGW 193  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 IVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDRGW 120

QY 194 AKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSH 253  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 AKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSH 180

QY 254 TLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLDPDQDATYFGAFKV 313  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 TLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLDPDQDATYFGAFKV 240

QY 314 RDID 317  
 ||||  
 Db 241 RDID 244

# RESULT 5

Q7ZYX9

ID Q7ZYX9 PRELIMINARY; PRT; 317 AA.  
 AC Q7ZYX9;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tnfsf10l protein.  
 GN Name=tnfsf10l;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=Whole body;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=Whole body;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC044336; AAH44336.1; -.  
 DR HSSP; P50591; 1D2Q.  
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 15.8%; Score 266; DB 2; Length 317;  
 Best Local Similarity 26.6%; Pred. No. 4.1e-14;  
 Matches 79; Conservative 66; Mismatches 122; Indels 30; Gaps 9;

Qy 42 PAASR-----SMFVALLGLGLG--QVVCSSVALFFYFRAQMDPNRISEDGTHCIYRILRL 93  
 || || ::||: : : | : : || | | :: | || |  
 Db 24 PANSRGRDSPSKLWIAMVVVVVVLQIASTTGLEFVYL--NMSLSQVKSQGVTEELRCLGL 81  
 Qy 94 HENADFQD TTLESQDTKLIPDSCRRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLD 153  
 | :| : :| :| :: : : : | : | :| :  
 Db 82 -LNLVGLKDQDIPEDLAQLFG EPCMKLAEGIKAYISKVTD SIISKQTLHAARTRTHSYNTT 140  
 Qy 154 LAK-RSKLEAQPF AHLTINATDIPS-----GSHKVSLS SWYHDRGWAKISN 198  
 :| : : :| |||::: | : : :| : | :|  
 Db 141 GSKFMTTVMQRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLN 200  
 Qy 199 MTF SNGKLIVNQDGFYYLYANICFRHHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLM 256  
 || :||:| | ||| |||: : ||: | : : ||: : ||| | :  
 Db 201 MTLTNGRLRVPQDGRYYLYSQVYFRYPSPSDSQSSVSHQLVQCIYKKT SYLNPIQ--LL 258  
 Qy 257 KGGSTKYWSGNSEFHFYSINVG GFFKLRSGE EISIEVSNPSLLDPDQDATYFGAFKV 313  
 || || | : ::| : :| || | :||:| : : ||:| : : : :||| : :  
 Db 259 KGVGTKCWAPDAEYALHSVYQGGLFELRAGDEVFVS VSSPTMVYGEDSSSYFGAFRL 315



07T1F2

Query Match 15.7%; Score 265; DB 2; Length 304;  
Best Local Similarity 27.3%; Pred. No. 4.7e-14;  
Matches 82; Conservative 56; Mismatches 126; Indels 36; Gaps 12;

Qy	38	PHQPPAASRSMFVALLGLGLGQVVCVALFFYFRAQMDP--NRI SEDGTHCI--YRILRL	93
Db	3	PAGGPSAHTCGAVLVAALLQSVCAVITYIYFTNELKQLWDTYRSRGTA CLTGEELGDL	62
Qy	94	HENADFQDTTLESQDTKLIPDCRRIKQAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLD	153
Db	63	IQNL D---VVESKDR--VADPCWQVKWHLGKLIKMM SRI-----LQENMSAINGDRTQ	111
Qy	154	-LAKRSKLEAQP----FAHLTINATDIPSGSHKV-----SLSSWYHD-RGWAKISNM	199
Db	112	ALSRRDEPPQGPTLRIA AHLTGSSKRSSASPHNYLSYRGIGHKIH SWESSRRGHSFLYNV	171
Qy	200	TFSNGKLIVNQDGFYYLYANICFRHHET----SG--DLATEYLQLMVYVTKTSIKIPSSH	253
Db	172	ELWNGELVVPQTGFYYIYSQTYFRFRENED EDSGLLERIKNPKQLVQYIYKLT-NYPDPI	230
Qy	254	TLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPDQDATYFGAFKV	313
Db	231	LLMKSARTSCWSKKA EYGLYSVYQGGV FQLKREDRI FVSVSNSDIVDMDKEASFFGAFMI	290

RESULT 7

TN10\_HUMAN

ID TN10\_HUMAN STANDARD; PRT; 281 AA.

AC P50591;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 10 (TNF-related

DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).

GN Name=TNFSF10; Synonyms=TRAIL, APO2L;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96111955; PubMed=8777713;

RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,

RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,

RA Goodwin R.G.;

RT "Identification and characterization of a new member of the TNF family

RT that induces apoptosis.";

RL Immunity 3:673-682(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=96278649; PubMed=8663110;

RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,

RA Ashkenazi A.;

RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor

RT necrosis factor cytokine family.";

RL J. Biol. Chem. 271:12687-12690(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
 RX PubMed=10542098; DOI=10.1038/14935;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Screaton G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.  
 RX MEDLINE=99413670; PubMed=10485660;  
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,  
 RA Sung Y.C., Oh B.-H.;  
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with  
 RT selective antitumor activity.";  
 RL Immunity 11:253-261(1999).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
 CC may be modulated by binding to the decoy receptors  
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
 CC induce apoptosis.  
 CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per  
 CC trimer.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Widespread; most predominant in spleen, lung  
 CC and prostate.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U37518; AAC50332.1; -.  
 DR EMBL; U57059; AAB01233.1; -.  
 DR EMBL; BC032722; AAH32722.1; -.  
 DR PDB; 1D0G; X-ray; A/B/D=114-281.  
 DR PDB; 1D2Q; X-ray; A=114-281.  
 DR PDB; 1D4V; X-ray; B=119-281.  
 DR PDB; 1DG6; X-ray; A=91-281.  
 DR PDB; 1DU3; X-ray; D/E/F/J/K/L=114-281.  
 DR Genew; HGNC:11925; TNFSF10.  
 DR MIM; 603598; -.



```

Qy      200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQLMVYVTKTSIKIPSSHTLMKGG 259
      ||::: ||::: || | : ||:: | : | ||
Db      168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMKSA 226

Qy      260 STKYWSGNSEFHFYSINVGGEFFKLRSGEESISIEVSNPSSLDPDQDATYFGAFKV 313
      || ::: || | ||:: : | : || | : | ::: || |
Db      227 RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280

```

RESULT 8

CAG33176

```

ID      CAG33176      PRELIMINARY;      PRT;      281 AA.
AC      CAG33176;
DT      01-JUN-2004 (TrEMBLrel. 27, Created)
DT      01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT      01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE      TNFSF10 protein.
GN      TNFSF10.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT      "Cloning of human full open reading frames in Gateway(TM) system entry
RT      vector (pDONR201).";
RL      Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; CR456895; CAG33176.1; -.
SQ      SEQUENCE      281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;

```

Query Match 14.9%; Score 251.5; DB 2; Length 281;  
Best Local Similarity 24.1%; Pred. No. 5.9e-13;  
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy	42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF	99
	: :: :   :   :   :   :   :   :   :	
Db	10 PSLGQTCVLIVIFTVLLQSLCAVTVYVFTNELKQM QDKYSKSGIACF-----LKED---	61
Qy	100 QD TTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSK	159
	: :   : :   :   :   :   :   : : : :	
Db	62 -DSYWDPNDEESMNSPCWQVKW-----QLRQLVRKMILTSEETI-----STVQEKKQ	107
Qy	160 LEAQPF-----AHLT-----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM	199
	: :   :   : :   :   :   :   :   :	
Db	108 QNISPLVRERGPQRVA AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRGHSFLSNL	167
Qy	200 TFSNGKLIVNQDGFYYLYANICFRHHETS GDLATEYLQLMVYVT KTSIKIPSSHTIMKGG	259
	: : : :   : :   :   : :   :   :   :   :	
Db	168 HLRN GELVIHEKG FYYIYSQT YFRFQEEIKENTKN DKMQMVQY IYKYT-SYPDPILLMKSA	226
Qy	260 STKYWSGNSEFH FY SINVG GF FKL RSGE EISIEVS NPSLLDPDQDATYFGAFKV	313
	: : :   :   :   :   :   :   :   :   :   :	
Db	227 RN SCWSKD AEYGLYSIQGGIFELKENDRIFVSVT NEHLIDMDHEASFFGAFLV	280

RESULT 9

Q6DHG9

ID Q6DHG9 PRELIMINARY; PRT; 299 AA.  
AC Q6DHG9;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Whole;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Whole;  
RA Strausberg R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC076005; AAH76005.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 299 AA; 33526 MW; BA776793D2F11ED5 CRC64;

Query Match 14.8%; Score 249.5; DB 2; Length 299;  
Best Local Similarity 28.1%; Pred. No. 9.5e-13;  
Matches 85; Conservative 49; Mismatches 126; Indels 43; Gaps 13;

Qy 44 ASRSM-FVALLGLG--LGQVVCVALFFYFRAQMDPNR--ISEDGTHCIYRI-LRLHENA 97  
:| :| :: || | | : | || : : |: | || :  
Db 6 SSHTMQYIGLLLLLAAILLQTIHAVVTFIYFSNVLSTMKETFSKSSVSCIMRANLRTIKQ 65  
Qy 98 DFQDTTLESQDTKLIPDSCRRIKQ-----AFQGA VQKELQHIVGSQHRAEKAMVDG 149  
: | :| | | :: | : ||| : | : | ::|  
Db 66 ELNGA--EGKD----DPCWQVTQQLHFLIEKSMSSRYQKEITSAVKDEVSRVLP SLVIQ 118

Qy	150	SWLDLAKRSKLEAQPF	AHLTINATDIPSG--SHKV---	SLSSWYHDRGWAKISNMTFSNG	204
		:     :	: :     :     :     :     :		
Db	119	DQED-SSRPKIAAHVTG	SYTPESEKDGAGLPNRKVY	GQKIQSWESEKGLAFLQ	NVELSDG 177
Qy	205	KLIVNQDGFYYLYANIC	FRH---HETSGDLATEY-----	LQLMVYVTKTSIKIP	250
		:   :         :	:     :   :		
Db	178	ELVVPQAGLYIYSQTY	FRHTLIEEDESAREDEY	GSMGESVRGKPMQYVY	KKVSSYQVP 237
Qy	251	SSHTLMKGGSTKYWSG	NSEFHFYSINVG	GFFKLRSGE	EISIEVSNPSLLDPDQ
		:   :	:   :   :	:   :   :	
Db	238	I--LLMKNARTTCWSR	DSEYGLYSIQAGL	FQLGSGDRVFVTVSN	VSTIDMDEKSSFFGA 295
Qy	311	FKV 313			
Db	296	FLV 298			

## RESULT 10

TN10 MOUSE

ID TN10 MOUSE STANDARD; PRT; 291 AA.

AC P50592;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 10 (TNF-related

DE apoptosis inducing ligand) (TRAIL protein).

GN Name=Tnfsf10; Synonyms=Trail;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96111955; PubMed=8777713;

RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,

RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,

RA Goodwin R.G.;

RT "Identification and characterization of a new member of the TNF family

RT that induces apoptosis.";

RL Immunity 3:673-682 (1995).

CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,

CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity

CC may be modulated by binding to the decoy receptors

CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot

CC induce apoptosis.

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Widespread.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC -----

DR EMBL; U37522; AAC52345.1; -.  
DR HSSP; P50591; 1D2Q.  
DR MGD; MGI:107414; Tnfsf10.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
KW Apoptosis; Cytokine; Signal-anchor; Transmembrane.  
FT DOMAIN 1 17 Cytoplasmic (Potential).  
FT TRANSMEM 18 38 Signal-anchor for type II membrane  
FT protein (Potential).  
FT DOMAIN 39 291 Extracellular (Potential).  
FT CARBOHYD 52 52 N-linked (GlcNAc... ) (Potential).  
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.7%; Score 248; DB 1; Length 291;  
Best Local Similarity 25.4%; Pred. No. 1.2e-12;  
Matches 79; Conservative 52; Mismatches 100; Indels 80; Gaps 13;

Qy 46 RSMFVALLGLG-LGQVVCVSVALEFFYFRAQMD--PNRISEDGTHCIYRILRLHENADFQDT 102  
| | : : : | | | : | | : | : | | : : | | :  
Db 17 RMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-----TDEDFWDS 71  
  
Qy 103 TLESQDTKLIPDSCRIK-----QAFQ-----GAVQKEL 131  
| | : : : | : : | : | | | | | | | |  
Db 72 T----DGEILNRPCLOVKRQLYQLIEEVTLRFTQDTISTVPEKQLSTPPLPRGGRPQKVA 127  
  
Qy 132 QHIVGSQHIRAEKAMVDGWSWLDLAKRSKLEAQPFHAHLTINATDIPSGSHKVSLSWYHDR 191  
| | | | : : : | : : : : | | | | : | | |  
Db 128 AHITGITR-RSNSALI-----PISKDGKTLGQ-----KIESWESSR 162  
  
Qy 192 -GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL-----QLMVYV 242  
| : : : : | | : : : | : | | : : | | | | : : : | : : :  
Db 163 KGHSFLNHVLFNRNGELVIEQEGLYIYSQTYFRFQEAED--ASKMVS KDKVRTKQLVQYI 220  
  
Qy 243 TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLDPD 302  
| : | | | | | : : : | | | | | : : : | : : : | : : |  
Db 221 YKYT-SYPDPIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLMDDL 279  
  
Qy 303 QDATYFGAFKV 313  
| : : : | | : : :  
Db 280 QEASFFGAFLI 290

#### RESULT 11

Q9DDZ5

ID Q9DDZ5 PRELIMINARY; PRT; 214 AA.  
AC Q9DDZ5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)



DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TRAIL-like protein.  
 GN Name=tnfsf101;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bobe J., Goetz F.W.;  
 RT "Molecular cloning and expression of a TNF receptor and two TNF  
 RT ligands in the fish ovary."  
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
 DR EMBL; AF250041; AAG47640.1; -.  
 DR HSSP; P50591; 1D2Q.  
 DR ZFIN; ZDB-GENE-010801-1; tnfsf101.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 14.3%; Score 240.5; DB 2; Length 214;  
 Best Local Similarity 28.6%; Pred. No. 3.5e-12;  
 Matches 61; Conservative 50; Mismatches 83; Indels 19; Gaps 5;

Qy 118 RIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAK-RSKLEAQPPFAHLTINATDIP 176  
 Db 2 KLAEGIKAYISKVTD SIISKQTLHAARTQTHSYNTTGSKFMTTVMQRPSAHLTLSSASDN 61  
 Qy 177 S-----GSHKVSLSWYHDRGWAKISNM TFSNGKLIVNQDGFYYLYANICF 222  
 Db 62 SRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLNMTLTNGRLRVPQDGRYYLYSQVYF 121  
 Qy 223 RHHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280  
 Db 122 RYPSPSDSDQSSVSHQLVQCIYKKT SYLNPIQ--LLKGVGTCWAPDAEYALHSVYQGGL 179  
 Qy 281 FKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313  
 Db 180 FELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212

# RESULT 12

Q90WT9

ID Q90WT9 PRELIMINARY; PRT; 287 AA.

AC Q90WT9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE TNF-related apoptosis inducing ligand-like protein.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bridgham J.T., Johnson A.L.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY057941; AAL23702.1; -.  
DR HSSP; P50591; 1D2Q.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006053; TNF\_abc.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 12.8%; Score 216.5; DB 2; Length 287;  
Best Local Similarity 24.7%; Pred. No. 5.7e-10;  
Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;

Qy 80 SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQH 139  
| : | : | : | : : : : : | | : : : | : : :  
Db 51 SSEELRCLQLINQQEGSNLEEL-----ISNQSLKLANTIKAYVATVTENVISRSV 102  
Qy 140 I-RAEKAMVDGSWLDLAKRSKLEAQPFALHTINATDIP-----SGSHKVSLSW 187  
: | : | : | : | : | : | : | : | : | : | : : : |  
Db 103 VNEAQKSYFNISEGQVA--TKTLGKPSAHLIFRPNPAQDGSSRRFGNLSQSCRHAITRW 160  
Qy 188 YHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVT-KTS 246  
: : | : | : | : | | | | | | : | : | : : : | : | :  
Db 161 EDSTIHSHLQNITYRDGRLRVNQAGKYVYSQIYFRYSRDGAGARVSVPLVQCINWKTS 220  
Qy 247 IKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDAT 306  
| : | : | : | : : : : | : | : : | : : | : : : | : :  
Db 221 YSQPI--LLLKGVGTCWAPAEYGLHALYQGGLFELKAGDELFSVSVSLAIDYSDAAS 278  
Qy 307 YFGAFKV 313  
| | | | : :  
Db 279 YFGAFRL 285

# RESULT 13

Q8K3G0

ID Q8K3G0 PRELIMINARY; PRT; 287 AA.  
AC Q8K3G0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE TNF-related apoptosis inducing ligand.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DA;  
 RA Mueller A.M., Giegerich G.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY115578; AAM49797.1; -.  
 DR HSSP; P50591; 1D2Q.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; UNKNOWN\_1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 12.8%; Score 215.5; DB 2; Length 287;  
 Best Local Similarity 24.2%; Pred. No. 6.9e-10;  
 Matches 73; Conservative 59; Mismatches 113; Indels 57; Gaps 14;

Qy 42 PAASRSMFVALLGLGLQVV---CSVAL-FFYFRAQMD--PNRISEDGTHCIYRILRLHE 95  
 | : | : : : | || : : || : : | : | : |  
 Db 10 PSFSQHFTMTVICIVLLQVLLQALTVAVTYMYFNNEVKQLQDNYSKIGLACFSK-----E 64  
  
 Qy 96 NADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRA-EKAMVDGSWLDL 154  
 : || || : | : : | : || : : : | || :  
 Db 65 DGDFWDST----DEGILNRCLQVK-----RQLYQLIEEVTLRTEKT-----IST 106  
  
 Qy 155 AKRSKLEAQP-----AHLT-----INATDIPSGSHKVSL----SSWYHD-RGWA 194  
 : | | : || : | || : : | : | : || :  
 Db 107 VPEKQLSTPPLPRGRRPQ RVAAHITGITRRSNLALIPISKDGKTLGQKIETWESSRRGHS 166  
  
 Qy 195 KISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLAT-----EYLQLMVYVTKTSIK 248  
 : : : || : : : || : : : | | | : : | :  
 Db 167 FLNHVHLRNGELVIQEEGLYYIYSQTYRFEAKEASKTVSKDGGRIKQMVQYIYKYT-S 225  
  
 Qy 249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLDPDQDATYF 308  
 | || | : | : || | : | : | : | : | : | :  
 Db 226 YPDPILLMKSAARNSCWSREAEYGLYSIQGGLFELKENDRIFVSVTNEHLMDLDEASFF 285  
  
 Qy 309 GA 310  
 ||  
 Db 286 GA 287

RESULT 14  
 TNF6\_PIG

ID TNF6\_PIG STANDARD; PRT; 282 AA.  
 AC Q9BEA8; Q95M04; Q95N10;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen  
 DE ligand).  
 GN Name=TNFSF6; Synonyms=FASL;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21322533; PubMed=11429161; DOI=10.1089/107999001300177493;  
 RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;  
 RT "Molecular cloning, characterization, and expression of porcine Fas  
 RT ligand (CD95 ligand).";  
 RL J. Interferon Cytokine Res. 21:305-312(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Guanxi bama miniature pig;  
 RA Zhu N., Young Y.;  
 RT "Molecular cloning and characterization of porcine Fas ligand cDNA.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphoid;  
 RA Tsuyuki S., Kono M., Bloom E.T.;  
 RT "Cloning and potential utility of porcine Fas ligand: overexpression  
 RT in porcine cells protects them from attack by human cytolytic cells.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;  
 RX MEDLINE=21653191; PubMed=11792426;  
 RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;  
 RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison  
 RT with human gene.";  
 RL Mol. Immunol. 38:581-586(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- INDUCTION: By IL-18.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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-----  
 DR EMBL; AB027297; BAB40919.1; -.  
 DR EMBL; AY033634; AAK56449.1; -.  
 DR EMBL; AF397407; AAK84408.1; -.  
 DR EMBL; AB069764; BAB64291.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Apoptosis; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.  
 FT CHAIN 1 282 Tumor necrosis factor ligand superfamily  
 FT member 6, membrane form.  
 FT CHAIN 131 282 Tumor necrosis factor ligand superfamily  
 FT member 6, soluble form (By similarity).  
 FT DOMAIN 1 82 Cytoplasmic (Potential).  
 FT TRANSMEM 83 103 Signal-anchor for type II membrane  
 FT protein (Potential).  
 FT DOMAIN 104 282 Extracellular (Potential).  
 FT DOMAIN 4 70 Pro-rich.  
 FT DOMAIN 45 56 Poly-Pro.  
 FT SITE 130 131 Cleavage (By similarity).  
 FT DISULFID 203 234 Potential.  
 FT CARBOHYD 185 185 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 251 251 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 261 261 N-linked (GlcNAc. . .) (Potential).  
 FT CONFLICT 5 5 F -> L (in Ref. 4).  
 FT CONFLICT 57 57 T -> P (in Ref. 2).  
 SQ SEQUENCE 282 AA; 31756 MW; 6743DAA1145671FB CRC64;

Query Match 11.9%; Score 200; DB 1; Length 282;  
 Best Local Similarity 23.0%; Pred. No. 1.4e-08;  
 Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

Qy 22 PGAPHEGPLHAPPPAPHPQPPAA---SRSM-----FVA 51  
 || | | ||| | || || : ||  
 Db 37 PGRP--GQRRPPPPPPPPPPPTLLPSRPLPPLPPPSLKKKRDHNAGLCLLVMFFMVLVA 94  
 Qy 52 LLGLGLGQVVCSSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKL 111  
 |:||||| :| | | : : | |:| : |  
 Db 95 LVGLGLG-----MFQLFHLQKE-----LTELRESASQRHT----- 124  
 Qy 112 IPDCRRIKQAFQGA VQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFHAHLT-- 169  
 : | : :| :: :|| | : |||



Best Local Similarity 22.8%; Pred. No. 4.1e-08;  
 Matches 74; Conservative 40; Mismatches 98; Indels 113; Gaps 12;

```

Qy      20 GGPG----APHEGPLHAPPPAPHPAASRSM-----FVALLGLG 56
      | ||      | |      |||| | ||      :      |||:||||
Db      38 GRPGQRRPPPPPPPTLPPPPPPPLPPLPLPPLKTRRDHNTGLCLLMFFMVLVALVGLG 97

Qy      57 LGQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSC 116
      ||      :| | |      | | : : : | :
Db      98 LG-----MFQLFHLQ-----KELAELRESTSQKH----- 121

Qy     117 RRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLT--INATD 174
      | | : : | : : ||      | : ||| | :
Db     122 -----VASSLEKQIGQLNPPSEKR-----ELRKVAHLTGKPNRSR 156

Qy     175 IP SGSHK VSLSSWYH DRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATE 234
      ||      | | : | : : | | : | | : : : | | : :
Db     157 IP-----LEWEDTYGIALVSGVKYKKGGLVINDTGM YFVYSKVNFRGQSCN----NQ 204

Qy     235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKLRS GEE 288
      | || : : | | || : | | : : | : : | | | :
Db     205 PLNHKVYMRNS--KYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGAVFNLT SADH 255

Qy     289 ISIEVSNPSILLDPDQDATYFGAFKV 313
      : : || || : : | : || : :
Db     256 LYNVSELSLVSFEEKSTFFGLYKL 280

```

Search completed: November 8, 2004, 18:32:13  
 Job time : 194 secs